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Result
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Maximum Match 100%
Listing first 45 summaries
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1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH
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11:
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13:
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               Published Applications AA: *
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/ Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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US-09-894-924-1
US-09-895-727-2
US-09-877-156-17
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US-09-877-156-2
US-09-877-156-2
US-09-877-156-2
US-09-877-156-2
US-09-062-113-62
US-09-062-113-62
US-09-062-113-75
US-09-062-113-75
US-09-062-113-74
US-09-062-113-74
US-09-062-113-74
US-09-062-113-74
US-09-062-113-74
US-09-062-113-11
US-09-062-113-11
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1	-758-124-	- 1	US-09-935-727-6	US-09-840-707A-17	-09-894	US-09-896-096A-17	-09-826-21	779	US-09-062-113-67	74-	US-09-756-854-20	US-09-062-113-9	-7	US-09-840-795-11		US-09-062-113-63	4-592-	-60	-58	62-113-6	62-113-	US-09-062-113-64	-09-062-113-	US-09-062-113-73	US-09-062-113-79
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## ALIGNMENTS

RESULT 1 US-09-896-096A-1

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Sequence 1, Application US/09896096A

Patent NO. US20020061559A1

GENERAL INFORMATION:

APPLICANT: ASHKENAZI, AVI J

APPLICANT: BOTSTEIN, DAVID

APPLICANT: MODGE, KELLY H.

APPLICANT: KIM, KYUNG JIN

APPLICANT: LAWRENCE, DAVID A.

APPLICANT: ROY, MARGARET A

APPLICANT: TUMAS, DANIEL B

APPLICANT: WOOD, WILLIAM

APPLICANT: WOOD, WILLIAM

TITLE OF INVENTION: DCR3 POlypeptide, A TNFR Homolog

FILE REFERENCE: P1134R2 REVISED

CURRENT FILING DATE: 2001-06-28

PRIOR APPLICATION NUMBER: US 09/157,289

PRIOR APPLICATION NUMBER: US 60/059,288

PRIOR APPLICATION NUMBER: US 60/059,288

PRIOR APPLICATION NUMBER: US 60/094,640

PRIOR FILING DATE: 1998-07-30

NUMBER OF SECTION NUMBER: US 60/094,640

PRIOR FILING DATE: 1998-07-30
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                                                                                                                                                                                                                            ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-896-096A-1
                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 18
SEQ ID NO 1
LENGTH: 300
                                                                                                                                           Query Match
Best Local Similarity
Matches 271; Conserv
                       61
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                                                                                       1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR
YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
                                                                VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR
                                                                                                                                               Conservative
                                                                                                                                    100.0%; Su
100.0%; Pr
                                                                                                                                             Score 1491; DB 10;
Pred. No. 8.8e-107;
); Mismatches 0;
                                                                                                                                             Indels
                                                                                                                                                                                   Length 300;
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                                                                                                                         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
                               COPCPPGTFSASSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
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                                                     COPCPPGTFSASSSSSBQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAB
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BOISTEIN, DAVID
APPLICANT: BOISTEIN, DAVID
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: KIM, KYUNG JIN
APPLICANT: KIM, KYUNG JIN
APPLICANT: RITI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: ROY, MARGARET A
APPLICANT: ROY, MARGARET A
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POLYDEDLIGE, A TNFR HOMOLOG
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US 60/0894,924
CURRENT FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/089,640
PRIOR FILING DATE: 1998-07-30
NUMBER: OF SEQ ID NOS: 18
SEQ ID NO
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Pred. No. 8.8e-107;
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US-09-894-924-1
; Sequence 1, Application US/09894924
; Patent No. US20020005210A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
, APPLICANT: BOTSTEIN, DAVID
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US-09-894-924-1
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Best Local Similarity
Matches 271; Conserv
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APPLICANT:
APPLICANT:
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RESULT

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61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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                                                                                                                 APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454P2
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100.0%; Pred. No. 8.8e-107;
ive 0; Mismatches 0;
                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR PILING DATE: 2001-07-06
PRIOR PILING DATE: 2001-07-06
PRIOR PILING DATE: 2000-11-21
PRIOR PILING DATE: 2000-11-21
PRIOR PELLING DATE: 2000-08-25
PRIOR PELLING DATE: 2000-08-25
PRIOR PELLING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-03
PRIOR PILING DATE: 1099-08-03
PRIOR PLILNG DATE: 1999-08-03
PRIOR PLILNG DATE: 1999-08-02
PRIOR PELLING DATE: 1999-04-20
PRIOR PELLING DATE: 1999-04-27
PRIOR PELLING DATE: 1999-04-27
PRIOR PELLING DATE: 1999-04-27
PRIOR PELLING DATE: 1999-03-04
PRIOR PELLING DATE: 1999-03-12
PRIOR PELLING DATE: 1999-03-14
PRIOR PELLING DATE: 1999-03-15
PRIOR PELLING DATE: 1999-03-16
PRIOR PELLING DATE: 1999-03-16
PRIOR PELLING DATE: 1999-03-16
PRIOR PELLING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: 60/124,095
PRIOR PELLING DATE: 1999-03-18
PRIOR PELLING DATE: 1999-03-18
PRIOR PELLING DATE: 1999-03-18
PRIOR PELLING DATE: 1999-03-19
PRIOR PELLING DATE: 1999-03-10
PRIOR PELLING DATE: 1999-03-10
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Sequence 2, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
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Matches 271; Conservative
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LENGTH: 300
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FILE REFERENCE: 1408.003/200130-130-1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
                                                                                                                                                                                                                                                 FILE REFERENCE: SF0818K
CURRENT APPLICATION NUMBER: US/09/840,795
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 300
TYPE: PRT
                                                                                                                                          ; FEATURE:
, NAME/KEY: misc feature
; LOCATION: (79)
; OTHER INFORMATION: Xaa at residue 79 is undetermined.
US-09-840-795-2
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US-09-840-795-2
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; ORGANISM: Homo sapien
US-09-877-156-17
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APPLICANT: Murphy, Erin E.

APPLICANT: Mateson, Jeanine D.

APPLICANT: Bates, Elizabeth Esther Mary

APPLICANT: Gorman, Daniel M.

APPLICANT: Lebecque, Serge J.E.

TITLE OF INVENTION: Mammalian Genes; Related
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Best Local Similarity
Matches 270; Conserv
                                                                    Query Match
Best Local Similarity
Matches 268; Conserv
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                    VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPMTCGPCPPRHYTQFWNYLERCR
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                                                                    98.5%;
ilarity 98.9%;
Conservative
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Pred. No. 1.1e.
0; Mismatches
                                                                      0,
                                                                    Score 1469; DB 10;
Pred. No. 4.2e-105;
0; Mismatches 3;
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.1e-105;
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Sequence 20, Application US/09877156

Patent No. US20020055625A1

GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 20
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                                                                                                                                                                 Sequence 2, Application US/09877156
Patent No. US20020055625A1
GENERAL INFORMATION:
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                                                                     APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF THE AND THER FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 3.9e-72;
0; Mismatches 2
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APPLICANT: TSUDA, EISUKE
APPLICANT: YANO, KAZUKI
APPLICANT: YANO, KAZUKI
APPLICANT: YANO, KAZUKI
APPLICANT: YANO, KAZUKI
APPLICANT: YANO, WISOO20051969Aluyuki
APPLICANT: SHIMA, No. US20020051969Aluaki
APPLICANT: YASUDA, Tomonori
APPLICANT: MORINAGA, Tomonori
APPLICANT: HIGASHIO, Kanji
APPLI
61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPG 113
                                                             90 YCNVLCGEREBEBARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPG 142
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,113
FILING DATE: 17-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
LOCATION: 1..305
OTHER INFORMATION: /note= "OCIF-DDD1"
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APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FEB-1995
FRICH APPLICATION DATA:
APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
FRICH APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
FRICH APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNAY/AGENT INFORMATION:
NAME: MOORE, ROIDA P.
REGISTRATION NUMBER: 44,244
REFERENCE/DOCKET NUMBER: FJN-060DV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          Sequence 71, Application US/09062113; Patent No. US200200501969A1; GENERAL INFORMATION: APPLICANT: GOTO, Masaaki
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INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
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amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -21..0
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CITY: Boston
STATE: MA
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FEATURE:
                                                                                                                                                                                                           RESULT 9
US-09-062-113-71
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US-09-935-727-4

US-09-935-727-4

DETECT NO. US20202150593A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTATION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta FILE REFERENCE: FP4542

CURRENT APPLICATION NUMBER: US/09/935,727

CURRENT APPLICATION NUMBER: US/03/324

PRIOR APPLICATION NUMBER: 60/33,224

PRIOR APPLICATION NUMBER: 60/25,131

PRIOR PLING DATE: 2000-10-06

PRIOR PLING DATE: 2000-10-06

PRIOR PLING DATE: 2000-10-06

PRIOR PLING DATE: 2000-08-25

PRIOR PLING DATE: 2000-08-25

PRIOR PLING DATE: 1999-12-01

PRIOR PRIOR SPELICATION NUMBER: 60/146,371

PRIOR PLING DATE: 1999-08-12

PRIOR PLING DATE: 1999-04-27

PRIOR PLING DATE: 1999-04-27

PRIOR PLING DATE: 1999-04-27

PRIOR PLING DATE: 1999-04-27

PRIOR PLING DATE: 1999-03-04

PRIOR PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SQNTQCQPCPPGTFSASSSSSSQQQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 120
                                                                                                                                                                                                                                                                                                                                                                                                                          56 LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LERCRYCNVLCGEREBEARACHATHNRACRCRIGFFAHAGFCLEHASCPPGAGVIAPGTP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 VAETPIYYPWRDAETGERLVCAOCPPGTFVORPCRRDSPITCGPCPRHYTOFWNYLERCR 89
                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                              56.4%; Score 841; DB 10; Length 153; 100.0%; Pred. No. 1.4e-57; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 45.0%; Score 671; DB 10; Length 170; Best Local Similarity 100.0%; Pred. No. 1.4e-44; Matches 113; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 153
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 153; Conserv
SEQ ID NO 2
LENGTH: 153
TYPE: PRT
ORGANISM: human
                                                                                                                                                                       US-09-877-156-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SULT 8
-09-935-727-4
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                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/062,113
FILING DATE: 17-APR-1998
CLASSIFICATION:
                                 APPLICATION NUMBER: JP 549
FILING DATE: 20-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JI
APPLICATION STEEL 20-FEB-1996
                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: UEDA, Masatsugu
APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146
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                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPFGAGVIAFGTFSQNTQCQFC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GAQDGALLVRLLQALRVARMPGLERSVRE-----RFL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENSVORHIGHANLTFEOLRSLMESL-----PGKKVGAEDIEKTIKACKPSDQILKLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDIDLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
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125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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NAKAGAWA, No. US20020051969Aluaki
MORINAGA, Tomonori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOBAYASHI, Fumie
SHIMA, No. US20020051969Aluyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSUDA, Eisuke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOCHIZUKI, Shin'ichi
                                     MBER: PCT/JP96/00374
20-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masaaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kazuki
                                                                                                                 JP 207508/1995
                                                                                                                                                                             JP 54977/1995
US 08/915,004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
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                                                                                                                                                                                                                                                                                               Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 326;
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; OTHER INFORMATION:
US-09-062-113-62
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-062-113-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 41.2 Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acid
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                 APPLICANT:
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 EEAFFRF 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 ERAVIDF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MOORE, RONDA P.
REGISTRATION NUMBER: 44
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 LCGEREEBARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                COUNTRY:
                                                                             CITY: Boston
                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POPOLOGY:
                                                                                                                                                          LE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKSGIDVTLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
                                                                                                                                                                                                                                                                                                                                                                                           75,
                                                                                                                                                                                                                                                                                                                                                                             5, Application US/09062113
US20020051969A1
                                      MA
USA
                                                                                           E: Testa, Hu
125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 amino acids
                                                                                                                                                                                                                    SHIMA, No. US20020051969Aluyuki
YASUDA, Hisataka
NAKAGAWA, No. US20020051969Aluaki
MORINAGA, Tomonori
                                                                                                                                                                                       HIGASHIO,
                                                                                                                                                                                                                                                                                                              TSUDA, Eisuke
MOCHIZUKI, Shin'ichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide -21..0
                                                                                                                                                                                                                                                                               KOBAYASHI, Fumie
                                                                                                                                                                                                                                                                                                                                              GOTO, Masaaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                                                       Masatsugu
                                                                                                                                                                                                                                                                                                   Kazuki
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                                                                                                                                                        No. US20020051969Alel Proteins and Methods for Producing
the Proteins
                                                                                                             Hurwitz & Thibeault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "OCIF-C19S"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 401;
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65 LCGEREEBARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TUNAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POLYPEPTIGE, A TNFR Homolog
FITLE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/894,924
CURRENT PILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR PILING DATE: 1998-09-18
PRIOR PILING DATE: 1998-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 18
LENGTH: 293
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TUMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POlypeptide, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
29.5%; Score 440.5; DB 1
Best Local Similarity 41.2%; Pred. No. 9.2e-27;
Matches 77; Conservative 31; Mismatches 74
                                                                                                                                                                                                                        CURRENT APLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1998-07-30
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US-09-894-924-18
US-09-894-924-18
, Sequence 18, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DODGE, KELLY H.
GURNEY, AUSTIN L.
KIM, KYUNG JIN
LAWRENCE, DAVID A.
PITTI, ROBERT
ROY, MARGARET A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRCANISM: Homo sapiens
US-09-896-096A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Gaps
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          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: /note= "OCIF-CDD2"
US-09-062-113-75
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
JP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTONNEY/AGENT INFORMATION:
NAME: MOORE, ROING P.
REGISTRATION NUMBER: 44,244
REFERENCE/DOCKET NUMBER: FUN-060DV
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/09896096A
Petent No. US20020061559A1
GENERAL INFORMATION:
APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: GOOGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
                                                                                                                           UMBER: US/09/062,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide LOCATION: -21..0
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                                                                                                                                                                          FILING DATE: 17 CLASSIFICATION:
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RESULT 14
US-09-062-113-80
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Patent No. US20020051969A1
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                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION NUMBER: PCT/JP96/00374
FPILICATION NUMBER: PCT/JP96/00374
FPILICATION NUMBER: US 08/915,004
PRIOR APPLICATION NUMBER: US 08/915,004
PRIOR APPLICATION NUMBER: US 08/915,004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

**POT TCATION NUMBER: US/09/062,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: L. Boston
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NAME: MOORE, RONDA P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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ZIP: 02110
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                                                                                                                                                                                                                                                                  CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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Similarity 41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T: HIGASHIO, Kanji
INVENTION: No. US20020051969Alel Proteins and Methods for Producing
INVENTION: the Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09062113
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125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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HIGASHIO, Kanji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YASUDA, Hisataka
NAKAGAWA, No. US20020051969Aluaki
MORINAGA, Tomonori
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SHIMA, No. US20020051969Aluyuki
                                   20-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kazuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 440.5; DB 10; Pred. No. 9.2e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 72,
Patent No. U
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 248-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
          COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: Protein
LOCATION: 1..300
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: FJI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
                                                                                                                                                                                                                  APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: No. US20020051969A1el Proteins
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS: LENGTH: 321 amino acids
CURRENT APPLICATION DATA:
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                  COUNTRY: US
ZIP: 02110
                                                                                                                                    CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85
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                                                                                                                                                                     125 High St.
                                                                                                                  USA
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SHIMA, No. US20020051969Aluyuki
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MOCHIZUKI, Shin'ichi
                                                                                                                                                                                                                                                                                                          NAKAGAWA, No. US20020051969Aluaki
MORINAGA, Tomonori
                                                                                                                                                                                                                                                                                                                                               YASUDA,
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                Version
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APPLICATION NUMBER: US/09/062,113
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION NUMBER: UP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION NUMBER: UP 207508/1995
FILING DATE: 20-FEB-1996
PRIOR APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOOKE, RONDA PRIOR P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COCATION: 1.306 OTHER INFORMATION: /note= "OCIF-DDD2"
US-09-062-113-72
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3 65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124 5; Gaps 26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLXCSP 85 5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64 Query Match

29.5%; Score 440.5; DB 10; Length 327;
Best Local Similarity 41.2%; Pred. No. 1e-26;
Matches 77; Conservative 31; Mismatches 74; Indels 5; g ò ò

125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182 g

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183 ERAVIDF 189 ò

203 EEAFFRF 209

Search completed: January 6, 2003, 11:27:02 Job time : 37 secs

5.1.3

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Minimum DB
Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1900.DAT:*
               January 6, 2003, 11:15:31; Search time 61 Seconds (without alignments) 591.982 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133250620 residues
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and is derived score Pred. No. No. is the number of greater than or equal by analysis of the total score distribution er of results predicted equal to the score of t / chance to have being pr printed,

SUMMARIES

Result No.	Score	Query Match Length DB ID	Length	BG	ID	Description
1	1491	100.0	271	20	AAY42184	Human mFLINT #1 pr
N	1491	100.0	271	21	AAB19334	A mature human FAS
ω	1491	100.0	271	21	AAB19705	Human FAS ligand i
4	1491	100.0	271	21	AAY97247	M68 TNF receptor r
S.	1491	100.0	271	21	AAY96598	Human mature FLINT
6	1491	100.0	271	22	AAE03567	Human mature fas l
7	1491	100.0	271	22	AAB68044	Amino acid sequenc
8	1491	100.0	271	22	AAB68047	Amino acid sequenc
9	1491	100.0	271	22	AAB74465	Human FLINT mature
10	1491	100.0	271	23	AAE14578	Human mature FLINT

Human protease-res	T,	AAE14586	23	271	9	48	45
Human protease-res	Ä	AAE14584	23	271	9	48	44
Human protease-res		1458	23	271	9	48	43
Human mature FLINT		965	21	271	9	48	42
Human protease-res			23	271	۰	48	41
fa	Ï	035	22	271	99.7	48	40
re	Ŧ	AAE14581	23	271	99.7	1487	39
Human FLINT mature	Ï	AAB74467	22	7	9	48	38
mature f		AAE03571	22	271	9	48	37
8		97	21	271	9	48	36
Human colon cancer		374	22	341	0	49	35
Human tumour necro	#	208	23	300	00.	49	34
		AAE14579	23	300	00.	49	33
		090	22	300	00.	49	32
Human PRO212 polyp		œ	22	300	00.	49	31
Human NTR3. Homo		175	22	300	00.	49	30
Human FLINT native		AAB74466	22	300	00.	49	29
Human native fas l		AAE03568	22	300	00.	49	28
		659	21	300	00.	49	27
Human PRO212 prote		439	21	300	00.	49	26
		035	21	300	00.	49	25
M68 TNF receptor r	3	AAY97246	21	300	00.	49	24
	H	AAB03621	21	300	00.	49	23
	H	AAB33416	21	300	00.	49	22
PRO212	•	2405	21	300	00.	1491	21
soluble	·	8	21	300	00.	49	20
length hu		AAB19335	21	. 300	00.	49	19
Orphan receptor (H		AAW95082	20	300	00.	49	18
tumour necr	II.	AAW97749	20	300	00.	49	17
Human DcR3 polypep	H	18	20	. 300	00.	49	16
nmor	M.	AAY17479	20	300	00.	49	15
Human FLINT #1 pro	<b>H</b>	18	20	300	00.	49	14
Human lung TNF-rec		9	20	300	100.0	1491	13
tumou		w	19	300	00.	49	12
Amino acid sequenc	Aı	AAW66102	19	300	00.	1491	11

## ALIGNMENTS

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30-MAR-1998;
20-MAY-1998;
09-SEP-1998;
17-DEC-1998;
18-DEC-1998;
18-DEC-1998;
22-DEC-1998;
                                                                                                                                                                               Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL apoptosis; inflammation; cancer; diabetes; acute liver failure; sepsis; hepatitis; ischaemia-associated injury; hypercoagulation; reperfusion-associated injury; aplastic anaemia; differentiation; growth; myelodysplastic syndrome; pancytopenic condition; myocardial ischaemia.
                                                                                                                                                                                                                                                         Human mFLINT #1 protein sequence.
                                                                                                                                                                                                                                                                                                      AAY42184;
                                                                                                                                                                                                                                                                                                                          AAY42184 standard; Protein; 271 AA
                                                                                               30-MAR-1999;
                                                                                                                    07-OCT-1999
                                                                                                                                        WO9950413-A2
                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                 17-DEC-1999
                                                                                                                                                                                                                                                                                 (first
                   98US-0079856.
98US-0086074.
98US-0099643.
98US-0112577.
98US-0112573.
98US-0112933.
                                                                                               99WO-US06797
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FasL;

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chronic obstructive pulmonary disease; Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "optionally replaced with Asn"
                                                                               'note= "optionally replaced with Met"
                                                   Location/Qualifiers
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                          Homo sapiens
The present invention describes therapeutic applications of mature FLINT (mFLINT) for use in the treatment of acute liver failure. Mature FLINT (mFLINT) which is a member of the tumour necrosis factor receptor superfamily, is used for treating acute liver failure, inflammation of the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercoagulation (including use with thrombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder, Type I diabetes, cancer, cell damage to an innocent bystander tissue that is induced by a chemotherapeutic agent or therapeutic irradiation, treating haematopoietic progenitor cells that have been exposed to therapeutic radiation or chemotherapy, aplastic anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34 cell and preventing damage to a cardiac myocyte resulting from abnormal myocardial ischaemia. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis; tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis; acute respiratory distress syndrome; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
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                                                                                                                     Use of mature FLINT for treating acute liver failure, inflammation, cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic and proinflammatory activity
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                         Heuer JG;
I, Reidy CA;
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                         Hale JE, Heu
Noblitt TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A mature human FAS Ligand Inhibitory Protein (FLINT).
                        Gould KE,
J, Na S,
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                     Bumol TF, Dou S, Glasebrook AL, Gould
Hui KY, Kharitonenkov A, Mizrahi J, N
Song HY, Wang J, Wu X, Zuckerman SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB19334 standard; Protein; 271 AA.
                                                                                                                                                                             Claim 31; Fig 3; 99pp; English.
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Matches 271; Conservative
(ELIL ) LILLY & CO ELI.
                                                                               WPI; 1999-591319/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 AA;
                                                                                               N-PSDB; AAZ25377.
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                                                                                                    The present sequence represents a mature numan ray receptor Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature FLINT protein is modified to produce analogues, which have greater potency, longer in vivo half-lives, decreased aggregation, decreased absorption onto surfaces, increased solubility and improved ease of formulation. The FLINT analogue is useful for treating a patient suffering from disease or condition relating to abnormal apoptosis such as acute lung injury, acute respiratory distress syndrome, pulmonary fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-1999;
21-JUN-1999;
21-JUN-1999;
20-OCT-1999;
                                                                                                                                                                                                                                                            FAS Ligand Inhibitory Protein analogs useful for treating abnormal apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis, chronic obstructive pulmonary disease ulcerative colitis or Crohn's
                                                                                 Sequence
                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                Newton CM,
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                                                    Local
2000-656167/63.
DB; AAA75999.
                                                                                                                                                                                                                                1; Page 112-113;
                                                  Similarity
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                                                                                   271 AA
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99US-0140077.
99US-0140156.
99US-0160566.
2000US-0183398.
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Pred. No. 8.5e-115;
Mismatches 0;
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218..219
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            "optionally replaced by any naturally occurring amino acid, preferably Gln, Glu, Ala, Gly, Ser, Val, Tyr or Asn as given in Claims, 9, 10, 11, 12, especially Gln as given in Claims 13, 14, 15, 35 and 36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "optionally Claims 10,
                                                                                                                                  "optionally replaced by any naturally occurring amino acid, preferably Tyr given in Claim 9"
                                                                                                                                                                                                                                                                                           "optionally replaced by occurring amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                              "optionally replaced Claims 11 and 14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "optionally replaced Claims 11 and 14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "optionally replaced by Claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "optionally Claims 10,
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                                                                                                                                                                                                                                                                                                                                                   "optionally replaced occurring amino acid
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given in Claims
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11, 13 and 14"
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CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE

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The present sequence is that of human FAS ligand inhibitory protein FLINT mature protein. FLINT is a tumour necrosis factor receptor homologue that binds FAS ligand, preventing its interaction with homologue that binds FAS ligand, preventing its interaction with lands and is implicated in runaway apoptosis and inflammatory disease. FLINT also binds to LIGHT, a membrane-bound ligand, which may play a role in immune modulation and apoptosis.

The invention relates to novel FLINT analogues (see also AAB19706-09) that are resistant to proteolysis by trypsin-like proteases between positions 218 and 219 of the FLINT mature protein sequence. The analogues have amino acids substitutions in the region comprising amino acids substitutions in the region comprising residues 34, 36, 132, 194 and/or 196. Nucleic acids, vectors and transformed host cells for recombinant production of the analogues are claimed. FLINT conduction of the analogues introducing the required point mutations. The protease resistant FLINT analogues are used to prevent or treat acute lung injury, acute respiratory stress syndrome, ulcerative colitis, chronic obstructive pulmonary disease, pulmonary fibrosis, to inhibit T lymphocyte activation, and to facilitate organ preservation for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel protease resistant FAS ligand inhibitory protein analogues resistant to in vivo or in vitro proteolysis at amino acid position 218 of the mature protein, useful for treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1491; DB 21; Length 271; 100.0%; Pred. No. 8.5e-115;
/note= "optionally replaced by any naturally occurring amino acid"
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    occurring amino acid"
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                                                                                      Misc-difference 221 /note= "optionally replaced by
                                                                                                                                               Misc-difference 222 /note= "optionally replaced by
                                                                                                                                occurring amino acid"
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99US-0140073.
99US-0147071.
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N-PSDB; AAA88730.
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Best Local Similarity
Matches 271; Conserv
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                                     Misc-difference
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21-OCT-1999;
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The M68 protein is a member of a family of proteins which have roles in immune responses, cell death, cell proliferation and stimulation of cell differentiation. M68 lacks a transmembrane domain stimulation of cell differentiation. M68 lacks a transmembrane domain and is a secrete factor suggesting that it functions as a natural inhibitor for its ligand. The altered expression pattern of M68 in a multitude of tissues suggests that M68 may play a role in cancer by binding to its ligand and blocking apoptotic cell death induced by such a ligand. This anti-apoptopic role of M68 suggests that modulators of M68 will be useful in treatment of apoptosis-related diseases such as various forms of cancer and various bone disorders. M68 nucleic acids and proteins are therefore useful for treating conditions involving atypical apoptosis and for identifying cancer and other diseases associated with abnormal levels of
121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                  M68; tumour necrosis factor; TNF; programmed cell death; apoptosis; receptor; immune response; cell differentiation; ligand; cancer; bone disease; systemate lupus erythematosus; Hashimoto's thyroiditis; drave's disease; idiopathic myxodema; autoimmune diabetes; thrombotic thrombocytopenic purpura; multiple sclerosis; liver diseases; autoimmune gastritis; ulcerative colitis; glomerulonephritis; pulmonary fibrosis; heart failure; atherosclerosis; aplastic anaemis; myelodisplastic syndromes; osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human M68 nucleic acids and proteins which are part of the tumor necrosis factor receptor (TNFR) family, useful for identifying modulators that may be used to treat various diseases e.g. cancer, osteopozosis, Alzheimer's disease
                                                                             ECERAVIDEVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD
                                                                                                                                                                                                                                                                                                                                                                                                   M68 TNF receptor related protein (mature protein)
                                                                                                                                                            241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
                                                                                                                                     GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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99US-0172754.
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20-DEC-1999;
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Best Local S
Matches 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR; FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic; anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
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                   Use of mature FLINT for treating e.g. acute respiratory distress syndrome, ulcerative colitis or ischemic injury during organ
transplantation
                                                                                                       N-PSDB; AAA51077.
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30-MAR-1999;
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Best Local Similarity
Matches 271; Conserv
                                                                                                                                                                                                                 Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI; TWFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS; acute respiratory distress syndrome; pulmonary fibrosis; pP; therapy; chronic obstructive pulmonary disease; COPD; acute lung injury; goitre; rheumatoid arthritis; fibroproliferative lung disease; ischaemia; seppsis; fibroric lung disease; human immunodeficiency virus; HIV; osteoporosis; chronic renal failure; graft-vs-host disease; cutaneous inflammation; vascular leak syndrome; Helicobacter pylori infection; atherosclerosis; insulin dependent diabetes mellitus (IDM); inflammatory bowel disease; crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis; chemitarorofe; multiple sclerosis; cytostatic; nootropic;
                              Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can also be used to treat acute liver failure, inflammation of the liver, abnormal (hepatocyte) apoptosis, sepsis, disorders associated with inflammation, hepatitits, ischemia, hypercoagulation or reperfusion, damage to a cardiac myocyte resulting from abnormal myocardial ischaemia, Type I diabetes, cancer, damage to an innocent bystander tissue induced by a chemotherapeutic or therapeutic irradiation, aplastic anaemias, myelodysplastic syndromes and pancytopenic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating acute respiratory distress syndrome, treating or inhibiting ulcerative colitis, inhibiting ischemic injury during organ transplantation or for organ preservation during transplantation. mFLINT
                                                                                                                                      Homo
                                                                                                                                                                                                    neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE03567 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; Fig 3; 125pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mature fas ligand inhibitory protein (FLINT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                             Location/Qualifiers
   /note=
                                                                                                                                                                                                    vasotropic.
"N-linked glycosylation site"
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The present sequence is human mature fas ligand inhibitory protein CC (FLINT). FLINT, a homologue of tumour necrosis factor receptor correction of Pask with fas. ligand (Fask) and thereby preventing the interaction of Fask with fas. FLINT comprising O-linked or N-linked or N-linked or Oligosaccharides is useful for preventing or treating acute lung injury (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis, chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PP), to facilitate organ preservation for transplantation and to inhibit T or lymphocyte activation. FLINT is useful for treating and/or preventing diseases such as rheumatoid arthritis, fibroproliferative lung disease, fibrotic lung disease, acute lung injury, chronic renal failure, graft-vs-host disease, cutaneous inflammation, vascular leak syndrome, const disease, cutaneous inflammation, vascular leak syndrome, constance mellitus (IDDM), osteoporosis, inflammatory bowel disease, crohm's disease, sepais, pancreatitis, cancer, autoimmune disease such as postiasis, Down's syndrome, and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                     New FLINT polypeptide for treating and/or preventing acute lung injury, acute respiratory distress syndrome, ulcerative colitis, and graft-versus-host disease, comprises O-linked or N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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                                          /incte= "O-linked glycosylation site"
218..219
/note= "Proteolytic cleavage"
174
/note= "O-linked glycosylation site"
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                                                                                                                                                                                                                   99US-0169367.
99US-0169381.
99US-0169412.
                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191430
                                                                                                                                                                                   29-NOV-2000; 2000WO-US30166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 271; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           2001-381684/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligosaccharides -
                                                                                                                                                                                                                                                                                                                                           Witcher DR;
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                                                                                                                    WO200142463-A1
Modified-site
                                 Modified-site
                                                                   Cleavage-site
                                                                                                                                                                                                                         07-DEC-1999;
                                                                                                                                                                                                                                     07-DEC-1999;
07-DEC-1999;
                                                                                                                                                     14-JUN-2001
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The present sequence represents a mature FLINT (FAS Ligand Inhibitory Protein) polypeptide. The specification describers a composition comprising a divalent metal cation and FLINT protein. The composition is used either for reducing, reversing or eliminating aggregation and precipitation of FLINT or for inducing oligomerisation or aggregation of FLINT molecules. They can be used for purifying FLINT and/or maintaining FLINT in solution. The compositions are used to treat and/or prevent disorders associated with the binding of Fas to Fast and/or LIGHT to the LTbetaR and/or FRZ/HVEM receptors. Uses include the treatment of acute liver failure and cerebral ischemia and the prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compositions comprising a divalent metal cation and a FAS Ligand Inhibitory Protein (FLINT), for reducing or inducing aggregation of FLINT and for treating diseases involving FasL/Fas and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COPCPPGTFSASSSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
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0
                                                                                                                                                                                                                          FLINT, FAS ligand inhibitory protein, divalent metal cation, Fa
Fas ligand, acute liver failure, cerebral ischemia, apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                             Amino acid sequence of a human mature FLINT polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1491; DB 22; 100.0%; Pred. No. 8.5e-115;
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Example 1; Page 39-40; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR;
                                                                                             AAB68044 standard; Protein; 271
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                                                                                                                                                                                                                                                                                                                                                                                                       99US-0153339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tian Y,
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                                                                                                                                                              29-JUN-2001
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Matches 271;
                                                                                                                              AAB68044;
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Best Local S
Matches 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human mature FLINT (FAS Ligand Inhibitory Protein) polypeptide. The specification describers a composition comprising a divalent metal cation and FLINT protein. The composition is used either for reducing, reversing or eliminating aggregation and precipitation of FLINT or for inducing oligomerisation or aggregation of FLINT molecules. They can be used for purifying FLINT and/or maintaining FLINT in solution. The compositions are used to treat and/or prevent disorders associated with the binding of Fas to FasL and/or LIGHT to the LTDetaR and/or TR2/HVEM receptors. Uses include the treatment of acute liver failure and cerebral ischemia and the prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compositions comprising a divalent metal cation and a FAS Ligand Inhibitory Protein (FLINT), for reducing or inducing aggregation FLINT and for treating diseases involving Fast/Fas and/or LIGHT/LT-beta-R receptor interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-2000; 2000WO-US20805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a human mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-2001
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                                                                                             CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
                                                                                                                                                                                                            YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ
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ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD
                                                                                                                                                                                                                                                                                                                                                                                                          271;
                                                         CQPCPPGTF$ASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
                                                                                                                                                                        YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ
                                                                                                                                                                                                                                                                                             VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 1491; DB 22;
Pred. No. 8.5e-115;
0; Mismatches 0;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a composition comprising a divalent metal cation associated with a protease resistant Fas ligand inhibitory protein (FLINT) analogue. The composition is useful in the treatment of diseases associated with Fas binding to its ligand, such as acute liver failure, inflammatory diseases, cerebral ischaemia and apoptosis. The present sequence is the mature FLINT protein.
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                                                   ECERAVIDEVAFQDISIKRIQRILIQAIEAPEGWGPTPRAGRAAIQIKIRRRITEIIGAQD 240
                                                                                                                                                                                                                  CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSSHDTLCTSCTGFPLSTRVPGAE
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                                                                                                                                                                   CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1491; DB 22;
Pred. No. 8.5e-115;
; Mismatches 0;
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GALLVRLLQALRVARMPGLERSVRERFLPVH 271

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This is the amino acid sequence of the human tumour necrosis related receptor (TR4), used in the method of the invention. The TR4 protein or its agonist can be used to treat a subject in need of enhanced TR4 polypeptide activity. The antagonist is used to inhibit TR4 polypeptide activity. The active agents can be used for the treatment and prevention of diseases such as chronic and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation, arthritis, septicaemia, autoimmune diseases, transplant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA encoding tumour necrosis related receptor - used to treat and prevent e.g. inflammation, arthritis, septicaemia, autoimmune diseases, transplant rejection, infection, stroke, ischaemia, ARDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, tumour necrosis related receptor; TR4, agonist, antagonist, inhibition, chronic; acute; inflammation; arthritis; septicaemia; autoimmune disease; transplant rejection; stroke; cancer;
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CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
                                                                                         ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRLTELLGAQD
                                                                ECERAVIDEVAFODISIKRLORLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of tumour necrosis related receptor (TR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1491; DB 19; 100.0%; Pred. No. 9.6e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rejection, stroke, cancer, Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restenosis, AIDS, bone disorders and cancer
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                                                                                                                                                          GALLVRLLQALRVARMPGLERSVRERFLPVH 271
                                                                                                                                                                                      Truneh A, Young
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                AAW66102 standard; Protein; 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 21pp; English.
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Best Local Similarity
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AAW66102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a new method of administering FLINT analogs that involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog. The method enables systemic absorption of FLINT through lungs and significantly reduces or eliminates the need for administering FLINT by injection or other routes of administration. The method is useful in treating disorders related to enhanced apoptosis (e.g. organ failure in liver, kidneys and pancreas) and inflammatory diseases associated with neutrophil activation (e.g. sepsis, acute respiratory distress syndrome, acute lung injury, systemic inflammatory response syndrome (SIRS) and multiphe organ dysfunction (MODS)). The method minimises the pain and disconfort of injection methods. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog, useful for treating e.g. sepsis or respiratory distress syndrome, involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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                                                                                                                                                                                                                                                                                                              FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis; organ failure; liver; kidney; pancreas; inflammatory disease; neutrophil; sepsis; acute respiratory distress syndrome; acute lung injury; systemic inflammatory response syndrome; sultiple organ dysfunction; MODS; human.
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  241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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                                                                                                                                          Ą
                                                                                                                                          standard; Protein; 271
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                                                                                                                                                                                                                                                                             Human mature FLINT protein.
                                                                                                                                                                                                                                    (first entry)
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Matches 271; Conservative
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                                                                     The present sequence represents the human tumour necrosis factor receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides for the TNFR-6 beta protein (AAW63023). TNFR-6 alpha and TNFR-6 beta are members of the tumour necrosis factor receptor (TNFR) family. TNFRs are expressed in endothelial cells, keratinocytes, normal prostate and prostate tumour tissue. For a number of disorders of these cells, particularly of the immune system, substantially altered (whether increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta polypeptides, nucleic acids and antibodies are claimed to be useful in the diagnosis of such disorders. Mutations of the TNFR 6 alpha and TNFR-6 beta genes can also be detected. The TNFR polypeptides are also claimed to be useful for identifying ligands which may be useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Fig 1; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human tumour necrosis factor receptors the diagnosis of immune system-related
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                                                   the treatment of apoptosis related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-399142/34.
DB; AAV39085.
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Sequence

300 AA;

This invention describes a novel tumour necrosis factor (TNF) receptor (I) isolated from human lung tissue. (I) is used: (i) to raise specific antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands

Claim 1;

Page 8-9;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy; detection; immunoassay; diagnosis; disease; immune system; tumour; osteogenic system; cardiovascular system; central nervous system; asthma; peripheral nervous systems; transplant incompatibility; antitumor; rheumatoid arthritis; antiasthmatic; antiarthritic.
                                                                                New soluble member of tumor necrosis factor receptor family, useful for identification specific modulators and for treating disease e.g. tumors
                                                                                                                    N-PSDB; AAZ09998
                                                                                                                                                    Kroeger B
                                                                                                                                                                                                   09-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                /*tag= a
/product= "TNF-receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1491; DB 19; 100.0%; Pred. No. 9.6e-115;
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expressed from a gene therapy vector) in conditions associated with a deficit of (1). Ab are used: (a) for qualitative or quantitative or deficit of (1). Ab are used: (a) for qualitative or quantitative or detection of (1) in standard immunoassays (for diagnosis of disease, or susceptibility, or for monitoring); and (b) as therapeutic inhibitors in cases where (1) is overexpressed. Nucleic acid (11) that encodes (1) is overexpressed. Nucleic acid (11) that encodes (1) is overexpressed. Nucleic acid (11) that encodes (1) is overexpressed on application assays; (C) as source of antiennes molecules or ribozymes; and (b) to produce transgenic animals (for studying (patho) physiology of (1)). Diseases possibly associated with under- or over-expression of (1) are those of the immune, osteogenic, cardiovascular and central or peripheral nervous systems, commons, transplant incompatibility, asthma and rheumatoid arthritis. The products of the invention have antitumor, antiasthmatic and antitumior, antiasthmatic and incurred the invention have antitumor, antiasthmatic and antiarthritic activity. This sequence represents the TNF-receptor of the
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                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, FLINT, mFLINT, OPG3, tumour necrosis factor receptor; FasL, apoptosis; inflammation, cancer, diabetes, acute liver failure, sepsis, hepatitis; ischaemia-associated injury; hypercoagulation, reperfusion-associated injury; aplastic anaemia, differentiation;
                                                                                                                                                                                                                                                                                                                                30 VAETPIYPWRDAEIGERLVCAQCPPGTFVQRPCRRDSPITCGPCPPRHYTQFWNYLERCR
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                                                                                                                                                                                                                                                         Length 300;
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myocardial ischaemia.
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                         100.0%; Score 1491; DB 20;
100.0%; Pred. No. 9.6e-115;
ive 0; Mismatches 0;
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Best Local Similarity
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09-SEP-1998;
17-DEC-1998;
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The present invention describes therapeutic applications of mature FLINT (mFLINT) for use in the treatment of acute liver failure. Mature FLINT (mFLINT), which is a member of the tumour necrosis factor receptor superfamily, is used for treating acute liver failure, inflammation of the liver, abnormal apoptosis, a disorder associated with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercogulation (including use with thrombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder, Type I diabetes, cancer, cell damage or damage to an therapeutic irradiation, treating heematopoietic progenitor cells that have been exposed to therapeutic radiation or chemotherapy, aplastic anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34+ cell and preventing damage to a cardiac mycorte progenitor cell or CD34+ cell and preventing damage to a cardiac mycorte progenitor cell or DM34+ cell and preventing damage to a cardiac mycorte progenitor mellong from abnormal myocardial ischaemia. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of mature FLINT for treating acute liver failure, inflammation, cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic and proinflammatory activity
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                                                                                                                                                                                                      Hale JE, Heuer JG;
Noblitt TW, Reidy CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD
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Similarity 100.0%; Pred. No. 9.6e-115;
71; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalian tumour necrosis factor receptor OPG-2.
                                                                                                                                                                                            Bumol TF, Dou S, Glasebrook AL, Gould KE,
Hui KY, Kharitonenkov A, Mizrahi J, Na S,
Song HY, Wang J, Wu X, Zuckerman SH;
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98US-0112703.
98US-0112933.
98US-0113407.
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                                                                                                                                    & CO ELI
                                                                                                                                                                                                                                                                                                                                       WPI; 1999-591319/50.
N-PSDB; AAZ25375.
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                                                                                                                                 (ELIL ) LILLY
                               18-DEC-1998;
22-DEC-1998;
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Matches 271;
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Query Match 100.0%; Score 1491; DB 20; Best Local Similarity 100.0%; Pred. No. 9.6e-115; Matches 271; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a mammalian tumour necrosis factor receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis factor receptor family, and can be used: (i) to raise specific antibodies (Ab), (ii) to treat osteopenic disorders associated with excessive osteoclast activity, e.g. primary osteoporosis, Paget's disease, hyperglycaemia of malignancy, or osteolytic metastases; (iii) for affinity purification of cognate ligands, and (iv) to screen for ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents such as soluble forms of the protein, are used to prevent, or reduce severity of, an immune response, and for treating cancer. They can also be used in diagnostic assays. The nucleic acid sequence encoding OPG-2 can be used as a probe to isolate related sequences from other species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-347693/29.
N-PSDB; AAX76052.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tumour necrosis factor family receptor OPG-2
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24-NOV-1997;
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                          GALLVRLLQALRVARMPGLERSVRERFLPVH 271
                                                                                                                                                      ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
                                                                                                                                                                                                                                                                                     CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
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                                                                                                                     ECERAVIDEVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD
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97US-0066446.
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Search completed: January Job time : 63 secs

6,

2003, 11:16:50

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Run

OM protein - protein search, using sw model

Copyright

Sequence: Title: Perfect score:

US-09-936-024-1

Scoring table:

BLOSUM62 Gapop 10.0 , 262574 seqs,

Gapext

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Total number of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

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   US-08-794-796-2
US-09-286-529-20
US-09-286-529-2
US-09-286-529-2
US-08-974-022-6
US-08-974-186-6
US-08-974-186-6
US-08-974-186-6
US-08-974-186-6
US-08-795-447A-6
US-08-795-445A-2
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US-08-795-447A-4
US-08-795-447A-4
US-08-795-447A-4
US-08-795-4468-4
US-08-795-4468-4
US-08-795-447A-4
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379.696 Million cell updates/sec
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US-08-794-796-2
; Sequence 2, Ap;
; Patent No. 588
                                                            ; MOLECULE TYPE: US-08-794-796-2
                                                                                                            TELEX:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corporatio
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,796
EIITUM CAPPLICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Emery,
                                                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEPHONE: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NTWNTO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tan, KB
APPLICANT: Truneh, Alem
APPLICANT: Young, Peter
TITLE OF INVENTION: Tumor Necrosis
TITLE OF INVENTION: TR4
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CORRESPONDENCE ADDRESS
                                                                                                TOPOLOGY:
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5. 5885800
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US-08-706-945D-142
US-08-706-945D-130
US-08-706-945D-130
US-09-042-785A-7
US-09-06-353A-4
US-09-573-986-4
US-08-853-29-2
US-08-850-000-2
US-08-477-347-3
US-08-476-862-2
US-08-974-022-48
US-08-795-445A-48
US-08-795-445B-48
US-08-795-446B-48
US-08-795-446B-48
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       Score 1491; DB 2
Pred. No. 3e-124;
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Sequence 141, App
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Sequence 130, App
Sequence 4, Appli
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Sequence 2, Appli
Sequence 4, Appli
Sequence 48, Appl
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Minimum DB Maximum DB

seq Seq

length: 0 length: 2000000000

Regult No.

Score 1491

Query Match 100.

Length

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1476.5 1034

Pred. No. score grea and is der

440.55 440.55

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; TYPE: PRT
; ORGANISM: human
US-09-286-529-2
                                                                                                                                  , ORGANISM: Homo
US-09-286-529-20
                                                             SOFTWARE: Far
SEQ ID NO 20
LENGTH: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-09-286-529-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210
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                                                                                                                      TYPE: PRT
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                                                                                                 61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
                                                                                                                    90 YCNVLCGEREEBARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
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                                                        30 VAETPIYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPITCGPCPPRHYIQFWNYLBRCR 89
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                               1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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Indels
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Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 20, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
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Mismatches
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Conservative
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LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapien
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Best Local Similarity
Matches 270; Conserv
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US-09-286-529-17
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Matches 271;
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TITLE OF INVENTION: NEW MEMBERS OF THE REFRENCE: 1409.003/200130.439C1
CURRENT APPLICATION NUMBER: U$/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                            Score 1034; DB 4;
Pred. No. 4.8e-84;
0; Mismatches 2;
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                                                                                                                FastSEQ for Windows Version 3.0
FILE REFERENCE: 1408.003/200130.439C1
CURRENT PEPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
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Patent No. 6297367
GENERAL INFORMATION:
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US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, Willaim J.
                                                                                                                                                                                                                                                                                                            69.3%;
ilarity 98.9%;
Conservative
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Best Local Similarity
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Best Local Similarity
Matches 179; Conserv
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CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: TITLE OF INVENTION:

Calzone, r.... Chang, Ming-Shi Chang, Ming-Shi Chang, Ming-Shi Chang, Ming-Shi Chang, Ming-Shi Chang, Ming-Shi Chang, Riversia (1988)

Lacey, David L.

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RESULT 6
US-09-042-785A-12
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                                                                                                                                                                                                     Sequence 12, Application US/09042785A Patent No. 6194151 GENERAL INFORMATION:
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Best Local Similarity
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                TITLE OF INVENTION: NOVEL MOLECULES OF THEREFOR AND USES THEREFOR
                                                                                                                                                                                         APPLICANT:
COMPUTER READABLE FORM:
                                                                                                                                     NUMBER OF SEQUENCES:
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       STALL.
COUNTRY: UC
02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
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                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                           EEAFFRF 209
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                              USA
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                                                                                                                                                              Busfield, Samantha J
VENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
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41.2%; Pred. No. 2.9e-31;
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Patent No. 6
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
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REFERENCE/DOCKET NUMBER: METELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 EEAFFRF 209
                                                                                                                                                                   ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland
CITY: Thousand Oaks
STATE: California
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                                                                                                                                COUNTRY: USA
ZIP: 91320-1789
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77; Conserv
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Calzone, Frank J.
Chang, Ming-Shi
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(617)742-4214
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Pred. No. 2.9e-31;
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Query Match
Best Local Similarity 41.2%
Matches 77; Conservative
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                  183 ERAVIDF 189
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US-08-974-186-6
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                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                              Query Match 29.5%; Score 440.5; DB 4
Best Local Similarity 41.2%; Pred. No. 2.9e-31;
Matches 77; Conservative 31; Mismatches 74
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Patent No. 6284728
GENERAL INFORMATION
APPLICANT: Lacey, David L.
APPLICANT: Cacone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARATTERISTICS:
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One Amgen Center Drive
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EIBM PC compatible
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REFERENCE/DOCKET UNMBER:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                            LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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ADDRESSEE: Amgen Inc
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US-08-795-447A-6
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                                                                                                                                     26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85
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  Length 401;
29.5%; Score 440.5; DB 4; Length 41.2%; Pred. No. 2.9e-31; ive 31; Mismatches 74; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
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APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
ITILE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
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APPLICATION NUMBER: 08/577,788
FILING DATE:
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RERERENCE/DOCKET NUMBER: J
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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nes 77; Conservative
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MOLECULE TYPE: protein
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Best Local Similarity
"hes 77; Conserve
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ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
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APPLICATION NUMBER:
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TYPE: amino acid
TOPOLOGY: linear
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CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                                               26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85
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                                                                                                                                                                      LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
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EEAFFRF 209
                                 ERAVIDE 189
                                                                     PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC
                                                                                                     PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C
                                                                                                                                          VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145
                                                                                                                                                                                                                                                 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV
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Chang, Ming-Shi
                                                                                                                                                                                                                                                                                      Conservative
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Lacey, David L.
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41.2%; Pred. No. 2.9e-31;
tive 31; Mismatches 74; Indels 5
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-1
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                                                                                                                                                   SOFTWARE: FastSEQ
SEQ ID NO 1
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Best Local Similarity
Matches 77; Conserv
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: McDonnell, Peter C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09153927A Patent No. 6297022
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/153,927A
CURRENT FILING DATE: 1998-09-16
EARLIER APPLICATION NUMBER: 60/061,334
EARLIER FILING DATE: 1997-10-08
                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/056,980
PRIOR APPLICATION NUMBER: 60/056,980
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS FILE REFERENCE: GH-50030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A Method of Identifying Agonists and TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TITLE OF INVENTION: and TR5 FILE REFERENCE: GH50031
                                                                                                                                                                                            PRIOR FILING DATE: 199
                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-08-26 PRIOR APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/072,993C CURRENT FILING DATE: 1998-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Michael R. APPLICANT: Peter R. 1
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TYPE: PRT
                                                                                                                               LENGTH: 401
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                                                                                                                                                                          Windows Version 3.0
29.5%;
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41.2%; Pred. No. 2.9e-31;
tive 31; Mismatches 74
                                                                                                                                                                                                                                          60/057,550
  Score 440.5; DB 4; Pred. No. 2.9e-31;
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RELATED RECEPTORS TR1
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NUMBER OF SEQUENCES:
                                                                 CITY: The
STATE: Ca
COUNTRY:
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US-08-795-445A-2
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STATE:
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                                                        26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85
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 5; Gaps
                                5 PIYPWRDAEIGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
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74; Indels
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41.2%; Pred. No. 2.9e-31;
tive 31; Mismatches 74
                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-706-945D-128
Sequence 128, Application US/08706945D
Patent No. 6369027
GENERAL INFORMATION:
APPLICANT: BOYJE, William
APPLICANT: Calzone, Frank
APPLICANT: Calzone, Frank
APPLICANT: Calzone, Frank
APPLICANT: Calzone, Frank
TILE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR FILING DATE: 1995-12-22
 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08974022;
Patent No. 6015938;
GANERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentin version 3.1
SEQ ID NO 128
LENGTH: 401
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Best Local Similarity 41.2%
....hes 77; Conservative
   Conservative
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   77;
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125 PPGTFSASSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
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                                                                                                                                                                                                                                               Version #1.30
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Patent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
                                                                                                                             ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 ERAVIDFVAFQDISIKRLQRLLQAL 207
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APPLICATION NUMBER: 08/577,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Amgen Inc.
1840 Dehavilland Drive
                       1: Amgen Inc.
1840 Dehavilland Drive
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 401 amino acids
amino acid
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MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc
                                  STREET: 1840 CTTY: Thousand Oaks
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Matches 81; Conserv
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ZIP: 91320-1789
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STREET: 18
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
SAPULICATION OF SEAT B.
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
FILING DATE:
FILIN
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Search completed: January 6, 2003, 11:21:35 Job time: 22 secs
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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO spool/US09936024/runat_06012003 111606 12123/app_guery.fasta_1.455
-Q=/cgn2 1/USPTO spool/US09936024/runat_06012003 111606 12123/app_guery.fasta_1.455
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFTX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODEL-LOCAL -OUTFMT=pto -NORM=ext -HARPSIZE=500 -MINLEN=2 -MAXLEN=200000000
-USER=US09936024 @CCN 1 187 @runat 06012003 111666 12123 -NCPUE 6 -ICPU=3
-NO_XLDXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPON=10 -XGAPOXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.

2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.

3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.

4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.

5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.

6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.
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SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981_DAT:*

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first 45 summaries
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## SUMMARIES

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ALIGNMENTS

RESULT 1
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DT 17-L
DT 17-L
DX
Huma
XX
Hu Human mFLINT #1 nucleotide sequence. 17-DEC-1999 AAZ25377 standard; (first entry) CDNA; 813 ВÞ

Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; Fash; apoptosis; inflammation; cancer; diabetes; acute liver failure; sepsis; hepatitis; ischaemda-associated injury; hypercoagulation; reperfusion-associated injury; applastic anaemia; differentiation; growth, myelodysplastic syndrome; pancytopenic condition: myocardial ischaemia; ss

Homo sapiens.

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AAA75999 standard; DNA; 813
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                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes therapeutic applications of mature FLINT (mFLINT), which is a member of the tumour necrosis factor receptor (mFLINT), which is a member of the tumour necrosis factor receptor the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercogqulation (including use with thrombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder Type I diabetes, cancer, cell damage or damage to an tinsue that is induced by a chemotherapeutic agent or therapeutic irradiation, treating haematopoietic progenitor cells that have been exposed to therapeutic radiation or chemotherapy, aplastic anaemia, myelodysplastic syndrome or a pancytopenic condition mFLINT is also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34 eall and preventing damage to a cardiac myocyte resulting free manormal myocardial ischaemia. The present sequence
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                                                                                                                                                                                                                                                                                                          Use of mature FLINT for treating acute liver failure, inflammation, cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic and proinflammatory activity
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Kharitonenkov A, Mizrahi J, Na S,
Wang J, Wu X, Zuckerman SH;
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Human, FAS Ligand Inhibitory Protein, FLINT; analogue; apoptosis; tumour necrosis factor receptor; acute lung injury; bulmonary fibrosis; acute respiratory distress syndrome; ulcerative colitis; chronic obstructive pulmonary disease; crom's disease; ss.
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AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTCGCTTGGAGCAC
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AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu
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04-AUG-1999;
20-OCT-1999;
21-OCT-1999;
20-DEC-1999;
26-JAN-2000;
The present sequence is that of cDNA coding for human FAS ligand inhibitory protein FLINT mature protein (see AAB19705). FLINT is a tumour necrosis factor receptor homologue that binds FAS ligand, preventing its interaction with FAS. This interaction is implicated in runaway apoptosis and inflammatory disease. FLINT also binds to LIGHT, a membrane-bound ligand, which may play a role in immune modulation and apoptosis. The invention relates to movel FLINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acute lung injury; acute respiratory distress syndrome; chronic obstructive pulmonary disease; pulmonary fibrosis; ulcerative colitis; therapy; organ transpantation; ss.
                                                                                                                                                                                                                                                                       Novel protease resistant FAS ligand inhibitory protein resistant to in vivo or in vitro proteolysis at amino a
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analogues (see also AAB19706-09) that are resistant to proteolysis by trypsin-like proteases between positions 218 and 219 of the FLINT mature protein sequence. Nucleic acids, vectors and transformed host cells for recombinant production of the analogues are claimed. FLINT cDNA is used as a template for introducing the required point mutations e.g. via PCR mutagenesis. The protease resistant FLINT analogues are used to prevent or treat acute lung injury, acute respiratory stress syndrome, ulcerative colitis, chronic obstructive pulmonary disease, pulmonary fibrosis, to inhibit T lymphocyte activation, and to facilitate organ preservation for transplantation (claimed).
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Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and prevents FasL-Fas interaction. Mature FLINT (MFLINT) inhibits FasL-Fas mediated apoptotic and pro-inflammatory activity. WFLINT is useful for treating acute respiratory distress syndrome, treating or inhibiting ulcerative collitis, inhibiting ischemic injury during organ transplantation or for organ preservation during transplantation. MFLINT can also be used to treat acute liver failure, inflammation of the liver, abnormal (hepatocyte) apoptosis, seppis, disorders associated with inflammation, hepatitis, ischemia, hypercoagulation or reperfusion, damage to a cardiac myocyte resulting from abnormal myocardial ischaemia, type I diabetes, caneer, damage to an innocent bystander tissue induced by a chemotherapeutic or therapeutic irradiation, aplastic anaemias, myelodysplastic syndromes and pancytopenic conditions.
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Use of mature FLINT for treating e.g. acute respiratory distress syndrome, ulcerative colitis or ischemic injury during organ
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Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI; TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
                                      Human mature fas ligand inhibitory protein (FLINT) cDNA.
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acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy; chronic obstructive pulmonary disease; COPD; acute lung injury; goitre; rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis; chronic renal failure; graft-vs-host disease; cutaneous.inflammation; vascular leak syndrome; Helicobacter pylori infection; atherosclerosis; insulin dependent diseates mellitus [pylori inflammatory bowel disease; Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis; Down's syndrome; multiple sclerosis; cytostatic; nootropic; neuroprotective; vasotropic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sepsis;
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Homo sapiens

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29-NOV-2000; 2000WO-US30166
                                                                                      WO200142463-A1.
                                                                                                                                                    /product= "Human mature fas ligand inhibitory protein
(FLINT)"
/note= "CDS does not include start and stop codon"
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07-DEC-1999; 07-DEC-1999; 07-DEC-1999; 23-MAR-2000; P-PSDB; AAE03567. Lu J, (ELIL ) LILLY & CO 2001-381684/40. Witcher DR; ; 99US-0169367. ; 99US-0169381. ; 99US-0169412. ; 2000US-0191430. ELI.

New FLINT polypeptide for treating and/or preventing acute lung injury, acute respiratory distress syndrome, ulcerative colitis, and graft-versus-host disease, comprises O-linked or N-linked

Example 1; Page 53; 60pp; English

The present sequence is human mature fas ligand inhibitory protein CC (FLINT) cDNA, FLINT, a homologue of tumour necrosis factor receptor CC protein (TNPR), binds fas ligand (FasL) and thereby preventing the CC interaction of FasL with fas ligand (FasL) and thereby preventing the CC oligosaccharides is useful for preventing or treating acute lung injury (ALI), acute respiratory distress syndrome (ARDS), ulcerative colicis, cc chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF), to facilitate organ preservation for transplantation and to inhibit T CC (MI), ischaemia, brain trauma/injury, human immunodeficiency virus (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft vs-tost disease, cuteneous inflammation, vascular leak syndrome, thost disease, cuteneous inflammation, vascular leak syndrome, thost disease, cuteneous inflammation, vascular leak syndrome, collabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease, cuteneous inflammatory bowel disease, sepsis, pancreatitis, cancer, autoimmune disease such as CC Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as

Sequence 813 BP; 122 2 298 C; 267 ဂ္ 126 Η, 0 other;

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Query Match:
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3.46e-77
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Matches:
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The invention relates to a new method of administering FLINT (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog. The method enables systemic absorption of FLINT through lungs and significantly reduces or eliminates the need for administering FLINT by injection or other routes of administration. The method is useful in treating disorders related to enhanced apoptosis (e.g. organ failure in liver, kidneys and pancreas) and inflammatory diseases associated with neutrophil activation (e.g. sepsis, acute respiratory distress syndrome, acute lung injury, systemic inflammatory response syndrome (SIRS) and multiple organ dysfunction (MODS)). The method minimises the pain and discomfort of injection methods. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Administering FLINT (FAS ligand inhibitory protein) or FLINT analog, useful for treating e.g. sepsis or respiratory distress syndrome, involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog -
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Mismatches:
Indels:
multiple organ dysfunction; MODS; human; gene;
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                                                                                                                   Location/Qualifiers
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The present invention describes therapeutic applications of mature FLINT (C (mpILINT), which is a member of the tumour necrosis factor receptor (mpILINT), which is a member of the tumour necrosis factor receptor c superfamily, is used for treating acute liver failure, inflammation of the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercoagulation (including use with thrombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder rissue that is induced by a chemotherapeutic agent or therapeutic irradiation, treating haematopoietic progenitor cells that the therapeutic adents and the progenitor cells that canaemia, myelodysplastic syndrome or a pancytopenic condition. mpILINT is also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte resulting from abnormal myocardial ischaemia. The present sequence
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TGCCAGCCGTGCCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG
                                                        AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu
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                  ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis
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The present sequence is the coding sequence of the human Fas ligand inhibitor (FLINT). The FLINT protein is involved in cell-specific approass, and can be used to treat inflammatory and autoimmune diseases cuch as rheumatoid arthritis, inflammatory bowel disease, fundated lifections diseases such as HIV-induced lymphopenia, fundanent viral cheaticis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated ulceration, ischaemia and reperfusion conditions including acute and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung injury and acute respiratory distress syndrome, congestive heart failure and atherosclerosis, and Alzheimer's and Parkinson's diseases, brain crauma and injury, chronic glomerulonephritis, osteoporosis, aplastic anaemia, myelodysplasia, ulcerative collitis, Down's syndrome, and multiple sclerosis. In addition, the gene and protein can be used to prevent apoptosis following organ transplantation.
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Novel monkey Fas ligand inhibitor polypeptides, useful for treat inflammatory or autoimmune disease such as rheumatoid arthritis, infectious diseases such as chronic hepatitis, and scheeperfusion conditions -
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30-MAR-1999;
20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                        FINNT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNPR; FasL; LIGHT; appoptosis; pro-inflammatory; hepatotropic; vasotropic; anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic; anti-inflammatory; antibacterial; immunosuppressive; ds.
        Human FLINY (also known as osteoprotegrin 3) is a new tumour necrosis factor receptor (TNFR) superfamily member, which bids Fast and LIGHT and prevents Fast-Fas interaction. Mature FLINY (mFLINY) inhibits Fast-Fas mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
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P-PSDB;
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Best Local Similarity:
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GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu
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Matches:
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Tumour necrosis factor receptor; TNFR-Galpha; TNFR-6beta; therapy; immune system-related disorder; inflammatory disease; immunosuppressive; bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; autility solerosis; Crohn's disease; autoimmune encephalitis; allergy; graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis; neuroprotective; antiarteriosclerotic; dermatological; asthmi; receptor;
                 TGTGGCCCGTGTCCCCCGCGCCCTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC
                                                                                                                             AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis
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CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg
                                                               TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis
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                                                                                                                                                                                                                                             HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human; tumour necrosis factor receptor; muscle disorder; bone mass; screening; muscle metabolism; binding agent; cognate ligand; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel orphan human receptor polypeptide and nucleic acid diagnostic reagents and for treatment of muscle disorders
                                                                                                                                                                                                                 Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.
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                              868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 900
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REGENERON PHARM INC
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Best Local Similarity:
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21-NOV-2000;
06-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human tumour necrosis factor receptor (TNFR)-
dalpha and 6beta protein and their corresponding nucleic acids. The
invention provides screening methods for identifying agonists and
antagonists of TNFR-6alpha and 6beta activity. The invention also
provides diagnostic and therapeutic methods for detecting and treating
immune system-related disorders. The method is useful for treating or
preventing an inflammatory disease or disorder selected from bowel
disease, encephalitis, atherosclerosis and psoriasis, an autoimmune
disease or disorder selected from systemic lupus erythematosus,
arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
and autoimmune encephalitis, graft versus host disease (GVHD), and an
allers Non
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161
                                                                                           tumor necrosis factor receptor, NTR3, useful for treating cancers, oke, anemia, obesity, rheumatoid arthritis and transplantation
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The present sequence encodes the tumour necrosis factor (TNF) receptor polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful for treating diseases such as acquired-immunodeficiency syndrome (AIDS

diseases,

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sick syndrome, haemorrhagic shock, hepatitis, insulin resistance, belower and prosy, loukaemia, meningitis, multiple sclerosis, myocardial ischaemia, obesity, rejection of transplanted organs, rheumatoid arthritis, septic shock syndrome, stroke, adult respiratory distress syndrome (ARDS), tuberculosis, and a number of viral diseases. The NTR3 polypeptide is beful for identifying or developing new (ant) agonists of NTR3. It may be used as an immunogen to which antibodies may be raised. NTR3 nucleic acid molecules may be useful as hybridisation probes in diagnostic assays to test, either qualitatively or quantitatively, for the presence of an NTR3 DNA or corresponding RNA in mammalian tissue or bodily fluid samples.
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diabetes mellitus, disseminated intravascular coagulopathy, erythroid
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The MGB protein is a member of a family of proteins which have roles in immune responses, cell death, cell proliferation and stimulation of cell differentiation. MGB lacks a transmembrane domain stimulation of cell differentiation. MGB lacks a transmembrane domain cand is a secreted factor suggesting that it functions as a natural implication for its ligand. The altered expression pattern of MGB in a multitude of tissues suggests that MGB may play a role in cancer by binding to its ligand and blocking apoptotic cell death induced by such a ligand. This anti-apoptopic role of MGB suggests that modulators of MGB will be useful in treatment of apoptosis-related clissases such as various forms of cancer and various bone disorders. MGB nucleic acids and proteins are therefore useful for treating conditions involving atypical apoptosis and for identifying conditions are the MGB indentifying cancer and other diseases associated with abnormal levels of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated human M68 nucleic acids and proteins which are part of the tumor necrosis factor receptor (TNFR) family, useful for identifying modulators that may be used to treat various diseases e.g. cancer, osteoporosis, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                      M68; tumour necrosis factor; TNF; programmed cell death, apoptosis; receptor; immune response; cell differentiation; ligand; cancer; bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis; Crave's disease; idiopathic myxodema; autoimmune diabetes; thrombocytopenic purpura; multiple sclerosis; liver diseases; autoimmune gastritis; ulcerative colitis; glomentulonephritis; pulmonary fibrosis; heart failure; atherosclerosis; aplastic anaemia; myelodisplastic syndromes; osteopogosis; Alzheimers disease; Parkinsons disease; stroke;
                  GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu
                                                                                                                                                                                                                                                                                         TNF receptor related protein coding sequence.
                                                                    ArgSerValArgGluArgPheLeuProValHis 271
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                                                                                                            are expressed in endothelial cells, keratinocytes, normal prostate and prostate tumour tissue. For a number of disorders of these cells, particularly of the immune system, substantially altered (whether increased or decreased) levels of TNPR-6 alpha and/or TNPR-6 beta gene expression can be detected, therefore the TNFR-6 alpha and TNPR-6 beta polypeptides, nucleic acids and antibodies are claimed to be useful in the diagnosis of such disorders. Mutations of the TNPR-6 alpha and TNPR-6 beta genes can also be detected. The TNPR polypeptides are also claimed to be useful for identifying ligands which may be useful in the treatment of apoptosis related disorders.
                                                                                                                                                                                                                            The present sequence represents the human tumour necrosis factor receptor-6 alpha (TNFR-6 alpha) CDNA. The invention also provides for the TNFR-6 beta CDNA (AAV39086). TNFR-6 alpha and TNFR-6 beta members of the tumour necrosis factor receptor (TNFR) family. TNFR
                                                                                        Sequence 1077
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Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta; ocular neovascularisation; solid tumour; malignancy; prostate cancer; breast cancer; colon cancer; diabetic retinopathy; microbial infection; pre-maturity macular degeneration; allergy; inflammation; tissue damage;
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                                                                                AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr
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This sequence encodes the human tumour necrosis factor receptor 6
alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA
and protein sequences can be used in the prevention, treatment and
diagnosis of diseases associated with inappropriate TNFR expression. The
nucleic acids, polypeptides, antibodies, agonists and antagonists against
them may be used for the treatment of a range of conditions such as
clisorders associated with neovascularisation (especially ocular
neovascularisation) (such as solid tumours and malignancies (e.g.
prostate cancer, breast cancer and colon cancer), diabetic retinopathy
and parasitic infections, bone disease (e.g. osteoporosis),
thyroid associated opthalmopathy tissue/cell damage, wounds, microbial
and parasitic infections, bone disease (e.g. osteoporosis),
characterise disorders (e.g. Alzheimer's disease),
neurodegenerative disorders (e.g. Alzheimer's disease),
disorders (e.g. graft rejection), rheumatism, liver disease,
autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative
            bone disease; osteoporosis; atherosclerosis; cardiovascular disease; beurodegenerative disorder; Alzheimer's disease; immune disorder; graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma; psoriasis; septic shock; ulcerative colitis; therapy; ds.
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 associated opthalmopathy; cell damage; parasitic infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TNFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human tumour necrosis factor receptor proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g. Alzheimer's disease, osteoporosis and graft rejection -
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P-PSDB; AAY90357.
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Best Local Similarity:
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                                                                                          Homo sapiens
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240 831	221 ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp	
220 771	201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly	
200 711	181 GluCysGluArgAlaVallleAspPheValAlaPheGlnAspIleSerIleLysArgLeu	
180	161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu	
160 591	141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis	
140 531	121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln	
120 471	101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln	
100 411	81 AsmArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis	
80 351	61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis	
60 291	41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg	
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   sapien
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2 0	388	R R	RP RC	RI.	R R	RR	감	RI	8	R X	R P	RR	감	2 R	R R R R R	RP	22	0 P	RA	R A	R RX	88	RN	88	စ္က ၀	g g	D D	DI.	123	SU	RES TR6									
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	and TNF	rausberg   bmitted (	QUENCE FRO	Submitted (NOV-	QUENCE FRO	] OC. Nact.	uster.";	verexpres dependent	derman A.	DLINE=201	QUENCE FRO	Biol. Che	perfamily	Yu KY., Kwo	SSUE=Prosi	OUENCE FRO	ture 396:	enomic am	ddard A.D	wd P., Hua dowski P.,	DLINE=990 tti R.M.,	SSUE=Feta		Mammalia; Eutheria; Primate NCBI_TaxID=9606;	mo sapien: karvota: 1	FRSF6B OR	mor necro	-JUN-2002	-JUN-2002	6B HUMAN	1 MAN		142.5 137.5	ω,			152.5 151.5	15	٦.	
SPECIFIC	FUNCTION: Decoy receptor for the and TNFSF6/Fast. Protects against	VOV-2001	M N.A.	N	FROM N.A.	Acad. S	ב ב ב	of gene	Gallow	22600; P	OM N.A.	em. 274:	(TR6) si	von B.,	cate;	OM N.A.,	599-703 (	plificat	Botst	ang A., I	Marster	l lung;	Z Z	theria;	etazoa:	DCR3 OR	sis fact	(Rel. 4)	(Rel. 4	STAN			9.6 9.2			0		00	0	
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cretec	for t	EMBT/C		EMBL/C		. 9/:1	0	in num	Liu O	55513;		36(199	LIGHT	fai Y	18771	ENCE (		decoy	shkena	rnev z	2321; awrenc			; Cata	: Crar	, Y	ins ao	nnotat	<u>д</u>	PRT;		ALI	TNR7_F	TR1A E	ZAN MC	TR23_N	TRLT_F	TR18_F	INR6 N	
ı. in fetal lung, brain	cytotoxic ligand apoptosis.	ank/DDBJ databas		EMBL/GenBank/DDBJ databas		1230-1235(2000).	10000	and its location in	., Austin C.P., Caskey C.T.;	Hilliard C A Lin		99).	apoptosi	, Kwon B.	•	DF 30-35.		for Fas		<u> գա</u>	oy M.,			Catarrhini; Hominidae;	••		σ	15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)	•	; 300 AA.		ALIGNMENTS	HUMAN RAT	BOVIN	ZAN MOUSE	NOUSE	MACFA	HUMAN	NOUSE	
and liver.	ls TNFS14/LIGHT	(D		es.			,	la four-gene		<			.B. ";	) ~. )				ligand in lung and		Z H	chkel F.C.,			Homo.	uteleostomi:	100).	B precursor (Decoy						답이	Bog		mus	mac hom	hom	anus	

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-!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
Detected in adult stomach, spinal cord, lymph node, trachea, spleen, colon and lung. Highly expressed in several primary tumors from colon, stomach, rectum, esophagus and in SW480 colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
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TURE.CYS 1.
TURE.CYS 2.
TURE.CYS 4.
BY SIMILARITY.
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ProDom; PD000771; TNFR c6; 1.

SMART; SM0208; TNFR; 3.

PROSITE; PS00552; TNFR NGFR 1; 2.

PROSITE; PS50050; TNFR NGFR 2; 2.

Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1491; DB 1;
Pred. No. 1.1e-110;
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                                                             SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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EMBL, AF134240; AAD25688.1; --
EMBL, AF217793; AAF33685.1; --
EMBL, AF217794; AAF33686.1; --
EMBL, AF217794; AAF3368.1; --
EMBL, BC121845; CAC03668.1; --
EMBL, BC121845; CAC03668.1; --
EMBL, BC121845; CAC03668.1; --
EMBL, BC017065; AAF17065.1; --
Genew, HGNC:11921; TNFKSF6B.
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Best Local Similarity 100.
Matches 271; Conservative
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                                                carcinoma cells.
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TISSUB=Kidney;

MEDLINE=9726201; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
"Osteoprotegerin: a novel secreted protein involved in the regulation
of bone density.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Lung cancer;
MEDLINE-98151033; PubMed=9492069;
MEDLINE-98151033; PubMed=9492069;
Vasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.;
"Identity of costeoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro.";
Endocrinology 139:1329-1337(1998).
                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                      T11B HUMAN STANDARD; PRT; 401 AA.
000300; 060236; O9UHP4;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             He Z_{-}Y_{-}, Yang G.-Z., Zhang W.-J., Wu X.-F.; "Cloning and expression of osteoprotegerin from Homo sapiens."; Acta Biochim. Biophys. Sin. 31:680-684 (1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K
"Cloning and characterization of the gene encoding human
osteoprotegerin/osteoclastogenesis-inhibitory factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda Morinaga T., Tsuda E., Higashio K.; "Characterization of monomeric and homodimeric forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245:382-387 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT ASN-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 254:685-691 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 22-36 AND 378-401.
MEDLINE=98238645; PubMed=9571159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98351569; PubMed=9688283;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 89:309-319(1997).
                                                                                                                                                                                                                      (Human)
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                      Homo sapiens
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RESULT 2
T11B_HUMAN
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specifically inhibits osteoclastogenesis.";

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ProDom; PD000771; TNFR c6; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 4.
SMART; SM00208; TNFR; 4.
PROSITE; PS50017; DEATH DOMAIN
PROSITE; PS50052; TNFR NGFR 1;
PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98269100; PubMed=9603945;
Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverm
Dul E., Appelbaum E.R., Bichman C., DiPrinzio R., Dodds R.A.,
James I.E., Rosenberg M., Lee J.C., Young P.R.;
"Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL,";
J. Biol. Chem. 273:14363-14367(1998).
                                                                                                                                                                                                       EMBL; AB008822; BAA32076.1; -.
EMBL; AB008821; BAA33076.1; -.
EMBL; BC030155; BAA330155.1; -.
EMBL; AF134187; AAF20168.1; -.
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hofbauer L.C., Neubauer A., Heufelder A.E.; "Receptor activator of nuclear factor-kappaB licosteoprotegerin: potential implications for the
                                                                                                                                                                                                                                                                                                                                                                                                                     use
                                                                                                                                                                                                                                                                                                                                                                                                                                    the
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Morinaga T., Higashio K.;
                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of malignant bone diseases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21395914; PubMed=11505389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of structural domains inhibitory factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98148058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION, AND MUTAGENESIS OF CYS-400
                                                                                                                                                                                                                                                                                                                                                                                                   modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                           InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR c6;
Pfam; PF00020; TNFR c6; 3.
                                                                                                                                                                      MIM; 602643;
                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney, liver, spleen, thymus, prostate, ovary, small intestine, thyroid, lymph node, trachea, adrenal gland, testis, and bone marrow. Detected at very low levels in brain, placenta and skeletal muscle. Highly expressed in fetal kidney, liver and lung. INDUCTION: Upregulated by increasing calcium-concentration in the medium and estrogens. Downregulated by glucocorticoids. PTM: N-glycosylated. Contains sialic acid residues. SIMILARITY: CONTAINS 4 TMFR-CYS REPEATS. SIMILARITY: CONTAINS 2 DEATH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RAKI/OPC ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PER 92.460-470(2001).
FUNCTION: Acts as decoy receptor for RANKL and thereby neutrality function in osteoclastogenesis. Inhibits the activation of its function in osteoclastogenesis apoptosis in vitro. Bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                              AB008822; BAA32076.1; -.
AB008821; BAA32076.1; JOINED.
                                                                                                                                                                                                                                                                                                                       U94332; AAB53709.1; -.
                                                                                                                                                                                                                                                                                                   AB002146; BAA25910.1; -.
                                                                                                                                                                                       HGNC:11909; TNFRSF11B
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; DEATH_DOMAIN;
; TNFR_NGFR_1; 2
; TNFR_NGFR_2; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9478964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Commun.
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                                 FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of human osteoclastogenesis
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008727;

15-JUN-2002

15-JUN-2002

15-JUN-2002
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MUTAGEN
CONFLICT
SEQUENCE
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SIGNAL
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SITE
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DOMAIN
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TISSUE=Embryonic intestine;
MEDLINE=97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.
Luethy R., Nguyen H.Q., Wooden S., E
                                                        Rattus norvegicus ()
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                  (Osteoprotegerin)
TNFRSF11B OR OPG.
                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily me
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                                               NCBI_TaxID=10116;
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                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                    ERAVIDF 189
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                                                                                                                                                                                                                                  PPGTFSASSSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C
                                                                                                                                                                                    EEAFFRF
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                                                                                                                                                                                                                                                                                                      PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV
                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                     263
401
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oa; Chordata;
ia; Rodentia;
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401 M
263 D
46040 MW;
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142
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DEATH 2.
INVOLVED IN
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N-LINKED
N-LINKED
K -> N.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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MISSING: ABOLISHES
D -> A (IN REF. 1).
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Pred. No. 8.7e-28;
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                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                        FTId=VAR
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C.R., Kelley
Bennett L.,
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(GLCNAC.
(GLCNAC.
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HES DIMERIZATION
                                                                                                                                                                                                                                                                                                                       74;
M., Chang
Boone T.,
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                  Euteleostomi;
                                                          Murinae; Rattus.
                                                                                                  precursor
Shimamoto
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                                                                                                                                                                                                                                                                                                                                 ong as its content is in no way noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEATH S. INDIMERIZATION (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                  its function. Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRALL and protect against apoptosis. TRALL binding blocks the inhibition of osteoclastogenesis (By similarity).
-: SUBCELMILAR LOCATION: Secreted (By similarity).
-: INDUCTION: Upregulated by osteopontin.
-: SIMILARITY: CONTAINS 2 DEATH DOMAINS.
    Sullivan J.,
Pattison W.,
                                                       "Ogreoprotegerin: a novel secreted protein involved in the regulation of bone density.";
Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
TUMOR NECROSIS FACTOR RECEPTOR
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee Suggs S., Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEC6A31F1D4E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUPERFAMILY MEMBER 11B.
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SIGNAL 1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; FF00020; TNFR c6; 4.

SMART; SW00005; DEATH; 1.

SMART; SW00006; DEATH; 1.

SWART; SW00208; TNFR; 4.

SWOSITE; PS50017; DEATH DOMAIN; FALSE NEG.

PROSITE; PS00652; TNFR NGFR 1; 1.

PROSITE; PS00652; TNFR NGFR 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH 1.
DEATH 2.
                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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InterPro, IPR001368; TNFR_c6.
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105
142
185
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401 AA;
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DOMAIN
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REPEAT
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"Osteoprofegerin reverses osteoporosis by inhibiting endosteal osteoclasts and prevents vascular calcification by blocking a process resembling osteoclastogenesis.";
J. Exp. Med. 192:463-474(2000).
-!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUB=Kidney;
STRAIN=BALB/C; TISSUB=Kidney;
SIMONE WS., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
Colomberoegerin: a novel secreted protein involved in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach, intestines and calvaria. Highly expressed in decidua and placenta,
                         PPGTFSASSSSSSCOOPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE -- C 182
LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoclastogenesis inhibitory factor (OCIF) in embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98382527; PubMed-9714833;
Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga
                                                                                                       146 PDGFFSGETSSKAPCRKHTNCSSLGLLLIQKGNATHDNV---CSGNREATQNCGIDVTLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J., Simonet W.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                precursor
                                                                                                                                                                                                                                                                                                                                                                                                         Tumor necrosis factor receptor superfamily member 11B pr
(Osteoprotegerin) (Osteoclastogenesis inhibitory factor)
INFRSF11B OR OPG OR OCIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                    Tilb_MOUSE STANDARD; PRT; 401 AA. 008712; 070202; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                              ERAVIDFVAFQDISIKRLQRLLQAL 207
                                                                                                                                                                                                    EEAFFRFAVPTKIIPNWLSVLVDSL 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure of the mouse
gene and its expression
Gene 215:339-343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and in embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of bone density
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-!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,

7

5; Gaps

Indels

86; DB 1; .3e-26

Query Match
28.5%; Score 425.5; D
Best Local Similarity 39.5%; Pred. No. 1.3eMatches 81; Conservative 33; Mismatches

Length 401;

PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64 26 PKYLHYDPETGRQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDYSYTDSWHTSDECVYCSP 85

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InterPro; IPkv...

InterPro; IPkv...

InterPro; IPkv...

InterPro; IPRo1368;

INTERPRO1368;

INTERPRO1
   Best Local Similarity
                           Query Match
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CARBOHYD
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                                                                                         SEQUENCE
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INDUCTION: Upregulated by TGF-beta and estrogens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91045991; PubMed-2172983; Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King Kohno T., Squires C.H., Thompson R.C., Vannice J.L.; Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.; "A second tumor necrosis factor receptor gene product naturally occurring tumor necrosis factor inhibitor."; Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor necrosis factor receptor superfamily member necrosis factor receptor 2) (p80) (TNF-R2) (p75) (Contains: Tumor necrosis factor binding protein 2 TNFRSF1B OR TNFR2 OR TNFBR.
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01-FEB-1991 (Rel. 17, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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Smith C.A., Davis T., Anderson D., Solam L., E
Dower S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines
                                                                                                                                                  "Two human TNF receptors have similar intracellular, domain sequences."; Cytokine 2:231-237(1990).
                                                                                                                                                                                                                         Brockhaus M.,
                                                                                                                                                                                                                                                                                                                                "Physical mapping and genomic Genomics 35:94-100(1996).
                                                                                                                                                                                                                                                                                                                                                                                 Brodeur G
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96299745; PubMe Beltinger C.P., White F Lepaslier D., Stallard
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Science 248:1019-1023(1990).
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Z., Loetscher H., Gubler U
aus M., Lesslauer W.;
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N. PubMed=2166946;
g K., Onasch M "
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hite P.S., Maris J.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- PTM: A soluble form (tunor necrosis factor binding protein 2) is produced from the membrane form by proteolytic processing.
-:- PHARMAGENITCHAL: Available under the name Enbrel (Immunex and Wyeth.Ayerst). Used to treat moderate to server rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNRR2 linked to an Immugalobulin Fc chain. It binds to TNR-alpha and blocks its interactions with receptors.
-:- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
-:- DATABBASE: NAME=ENROW, NOTE=CD guide CD120b entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
-:- DATABBASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
WWW="http://www.enbrelinfo.com/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFSFI/lymphotoxin-alpha.

SUBCELLULAR LOCATION: Type I membrane protein and secreted.

PTM: Phosphorylated; mainly on serine residues and with a very low level on threonine residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION.
MEDLINE=93016040; PubMed=1328224;
Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
Lipari M.T., Goeddl D.V.;
"Blochemical properties of the 75-kDa tumor necrosis factor receptor.
Characterization of ligand binding, internalization, and receptor
                                                                      MEDLINE=90110215; PubMed=2153136;
Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor-binding proteins purified from human
urine. Evidence for immunological cross-reactivity with cell surface
tumor necrosis factor receptors.";
                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H., "Structural basis for self-association and receptor recognition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i. FUNCTION: Receptor with high affinity for INFSF2/TNF-alpha and approximately 5-fold lower affinity for homotrimeric
                                                                                                                                                                                                                                                                                         Loetscher H., Schlaeger B.J., Lahm H.-W., Pan Y.-C.E., Lesslauer
Brockhaus M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                         "Purification and partial amino acid sequence analysis of tw
distinct tumor necrosis factor receptors from HL60 cells.";
J. Biol. Chem. 265:20131-20138(1990).
                                                                                                                                                                                                                                              SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
MEDLINE=91056048; PubMed=2173696;
Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 267:21172-21178(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99221490; PubMed=10206649;
                                                                                                                                                                                                J. Biol. Chem. 265:1531-1536(1990)
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AAC50622.1; JOINED.
AAC50622.1; JOINED.
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U52165; AAC50622.1; -.
U52156; AAC50622.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC50622.1;
AAC50622.1;
AAC50622.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 398:533-538(1999).
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U52158;
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EMBL;
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143 CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVA----IPGNASMDA 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 YIQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAG-----FCLEHAS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VAETPTYPWRDAETGE------RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRH 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUPERFAMILY MEMBER 1B, MEMBRANE FORM. TUMOR NECROSIS FACTOR BINDING PROTEIN EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
TURE-CYS 1.
TURE-CYS 3.
TURE-CYS 4.
BY SIMILARITY.
BY SI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 RA----GRAALQLKLRRRLTELLGAQDGALLVRLLQAL---RVARMP-GLERSVRERFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.8%; Score 340.5; DB 1; Length 461; 29.7%; Pred. No. 7.6e-20; ive 43; Mismatches 115; Indels 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSOUGS2; TNFR NGFR 1; 2.
PROSITE; PSSOUGS0; TNFR NGFR 2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Phosphorylation; Pharmaceutical; 3D-structure.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> P (IN REF. 5).
-> R (IN REF. 2 AND 5).
-> T (IN REF. 5).
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603D0AE1CD69ACBF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48291 MW;
                                                                                                                                                                                                                                                                                                                                InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                 Genew; HGNC:11917; TNFRSF1B
S63368; AAB19824.2;
M35857; AAA63262.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                           PIR, A35356, A35356.
PIR, A36007, A36007.
PIR, A36475.
PIR, B35010, B35010.
PIR, A23666, A23666.
                                                                                                                                                                                                                                     PDB; 1CA9; 12-APR-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 AA;
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23
258
288
39
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CONFLICT
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SEQUENCE
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TRANSMEM
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Matches
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RESULT 6 TRIB\_MOUSE

AAC50622.1; AAA36755.1;

M55994;

AAC50622.

U52163;

EMBL; EMBL; EMBL; EMBL; EMBL;

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Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.; Submitted (WAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha approximately 5-fold lower affinity for homotrimeric TNFSF1/lymphotoxin-alpha (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NOD;
Jacob C.O., Liu J.;
Submitted (JAN-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; Copeland recogning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
  DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=91187885; PubMed=1849278;
Lewis M., Tartaglia L.A. Lee A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TR1B_MOUSE STANDARD; PRT; 474 AA.

P25119; P97893;

01-MAY-1992 (Rel. 22, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

Tumor necrosis factor receptor superfamily member necrosis factor receptor 2) (TNF-R2) (p75).

TNFRSFIB OR TNFR2 OR TNFR-2.
                                                                                                                      Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                              EMBL; M60469; AAA39752.1; -.
EMBL; M59378; AAA40463.1; -.
EMBL; U39488; AAA85021.1; -.
EMBL; X87128; CAA60618.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-26 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-22
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                                                                                                   CHAIN
                                                                                                                                                                                                                                        ProDom;
                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                           SP; P19438; INCF.
D; MGI:1314883; Thfrafib.
cerPro; IPR001368; TNFR_c6.
am; PF00020; TNFR_c6; 4.
DDom; PD000771; TNFR_c6; 1.
ART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                          B38634; B38634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H., Chen E.Y., Goeddel D.V., and expression of cDNAs for two stactor receptors demonstrate one
                                                                                                                                PS00652; TNFR NGFR 1; 2.
PS50050; TNFR_NGFR_2; 3.
PS50050; TNFR_NGFR_2; 3.
    259
289
289
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TUMOR NECROSIS FACTOR RECEPT
SUPERFAMILY MEMBER 1B.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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Ol-UUN-1994 (Rel. 29, Created)
Ol-UUN-1994 (Rel. 29, Last sequence update)
Ol-UUN-1994 (Rel. 29, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 3
(Lymphotoxin-beta receptor) (Tumor necrosis factor r
protein) (Tumor necrosis factor C receptor).
LTBR OR TWFRSF3 OR TWFCR.
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                                                             Strausberg
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Mammalia; Butheria; Primates;
                                                                                                                                                                                                 Baens M., Chaffanet M., Cassiman J
"Construction and evaluation of a
                                                                                                                                                                                                                                             MEDLINE=93252381; PubMed=8486360;
                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                          SEQUENCE
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16:214-218(1993).
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
                                        EMBL/GenBank/DDBJ databases
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Pred. No. 3.
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                             MEDLINE=20261554; PubMed=10799510; Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A., Whitbeck J.C., Cohen G.H., Eisenberg N.J., Ware C.F.; Cohen G.H., Eisenberg N.J., Ware C.F.; Intellymphotoxin-bera receptor is necessary and sufficient for LIGHT-mediated apoptosis of tumor cells."; J. Biol. Chem. 275:14307-14315(2000).
J. Biol. Chem. 275:14307-14315(2000).
LTA and LTB and for TNPS14/LIGHT. Promotes apoptosis via TRAF3 and LTB, and for TNPS14/LIGHT. Promotes apoptosis via TRAF3 and TRAF5. May play a role in the development of lymphoid organs.
                                                                                                                                                         MEDLINE=99223511; PubMed=10207006; Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.; Wu cytoplasmic domain of the lymphotoxin-beta receptor mediates cell death in HeLa cells.";
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TURR-CYS 2.

TURR-CYS 3.

TURR-CYS 4.

BY SIMILARITY.

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Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR_N6F. 1; 2.
PROSITE; PS50056; TNFR_N6FR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
             Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C., Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.; "A lymphotoxin-beta-specific receptor."; Science 264:707-710(1994).
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TUMOR NECROSIS FACTOR RECEPTOR
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-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 4 INFR-CYS REPEATS.
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                                                                                                                                                                                                                                          J. Biol. Chem. 274:11868-11873 (1999)
  MEDLINE=94225209; PubMed=8171323;
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Genew; HGNC:6718; LTBR.
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Score 299.5; DB 1; Length 435; Pred. No. 1.2e-16;

20.1%;

Best Local Similarity

Query Match

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MEDITION.

Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;

Inimparised C-Jun animot terminal kinase activity and T cell

I. Exp. Med. 194:1441-1448(2001).

J. Exp. Med. 194:141-1448(2001).

J. Exp. Med. 194:141-148(2001).

J. Exp. Med. 194:141-141-148(2001).

J. Exp. Med. 194:141-148(2001).

J. Exp. Med. 194:141-148(2001).

J. Exp. Med. 194:141-148(2001).

J. Exp. Med. 194:141-148(2001).

J. Exp. Med. 194:141-148(194).

J. Exp. Med. 194:141-1414.

J. Exp. Med. 194:141-141.

J.
                                                                                                                                                                   PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEEC 182
                                                                                                                                                                                                                                                                                                          169 PCKAGHFONTSSPSARCOPHTRCENOGLVEAAPGTAOSDTTCKNPLE-PLPPEMSGTMLM 227
                                                             EPOHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMG-- 109
                                                                                                                             EEEARACHATHNRACRCRTGFFAHAGFCLE--H----ASCPPGA-GVIAPGTPSQNTQCQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor (TNFR-
ETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGER 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse DR6: mouse homolog of human TNFR-related death receptor-6
                                                                                                                                                                                                                                                                                                                                                                              220
                                                                                                                                                                                                                                                                                                                                                                                                                                           228 LAVLLPLAFFLLLATVFSCIWKSHPSLCRKLGSLLK--RRPQGEGPNPVAG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa
Minami M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c; TISSUE=Kidney;
Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
"Murine DR6: murine TNFR-related death receptor-6.";
submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                              183 ERAVIDFVAFQDIS------IKRLQRLLQALEAPEGWGPTPRAG
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSEPUS, 091XH9; Q91W77;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 21;
related death receptor-6) (Death receptor 6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF322069; AAG38115.1; -.
EMBL; AY043489; AAK74193.1; -.
EMBL; BC016420; AAH16420.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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SMART; SM00208; TNFR; 4.
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   183
                                  173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro;
                                                                                                  113
                                                                 126
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CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
                                                                                                                                                                                           TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:2151075; Tnfref21.
ERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTE 234
                                                                                                                                                                TYRHVDRTTGQVLTCDKCPAGTYVSEHCTNMSLRVCSSCPAGTFTRHENGIERCHDCSQP 112
                                                               PGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPL---STRVPGAEEC
                                                                                                CPWPMIERLPCAALTDRECICPPGMYQSNGTCAPHTVCPVGWGVRKKGTENEDVRCKQCA
                                                                                                                             CGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTOCOPCP
                                  RGTFSDVPSSVMKCKAHTDCLGQNLEVVKPGTKETDNVC----GMRLFFSSTNPPSSGTV
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                                                                                                                                                                                                                                 69;
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                                                                                                                                                                                                                                                 Similarity
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IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis;
                                                                                                                                                                                                                                                                                                 42
350
371
415
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133
173
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677
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29.7%;
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                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                              Score 288.5;
Pred. No. 1.4e
32; Mismatches
                                                                                                                                                                                                                                                                                                               DEATH.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARIT
BY SIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
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                                                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                               Length
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Prodom; PROMOTOTI; TNFR o6; 1.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 4.

PROSITE; PS50017; DEATH DOMAIN; 1.

PROSITE; PS50015; TNFR NGFR 1; 1.

PROSITE; PS50050; TNFR NGFR 2; 1.

Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                - FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
- SUBCILIVIAR LOCATION: Type I membrane protein (Probable).
- SUBCILIVIAR LOCATION: Type I membrane protein (Probable).
- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta, pancreas, lymph node, thymus and prostate. Detected at lower levels in lung, skeletal muscle, kidney, testis, uterus, small intestine, colon, spleen, bone marrow and fetal liver. Very low levels were found in adult liver and peripheral blood leukocytes.
- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan G., Bauer J.H., Haridas V., We Aggarwal B.B., Ni J., Dixit V.M., "Identification and functional chadmain-containing TMF receptor."; FEBS Lett. 431:351-356(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98378343; PubMed=9714541; MEDLINE=98378343; PubMed=9714541; Mang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member related death receptor-6) (Death receptor 6).
                                                                                                                                                                                              EMBL; BC017730; AAH17730.1;
EMBL; BC010241; AAH10241.1;
Genew; HGNC:13469; TNFRSF21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain, and Colon;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TR21_HUMAN
075509; Q96D86;
                                                                                                                                   InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                        EMBL; AF068868; AAC34583.1;
EMBL; AL096801; CAB75692.1;
                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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                                                                                                                                                                    SSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                           TNFR_c6; 4.
                                                                                                                          death; 1.
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                                                                                                                                                                                                 TNFRSF21
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                                                                                                                                                                                                                                                                                                  noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 HATHNRACRCRTGFFAHAGFCL----EHASCPPGAGVIA-PGTPSQNT------QCQP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 TSDRKAECRCQPGM----SCVYLDNECVHCEEBRLVLCQPGTEAEVTDEIMDTDVNCVP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 CPPGTFSASSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECE 183
                                                               Genomics 30:312-319(1995).

-!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing LTA and LTB, and for TINES14/LIGHT. Promotes apoptosis via TRAF3 and TRAF5. May play a role in the development of lymphoid organs (By similarity).
-!- SUBUNIT: Self-associates (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R EMBL; U29173; AAA68964.1; -.
R EMBL; U30798; AAB1334.1; -.
R EMBL; U30798; AAB1334.1; -.
R EMBL; U30798; AAB1334.1; -.
HSSP; O14763; LDD4.
R MGD; MGI:104875; Ltbr.
R Pfaur; PF000020; TNFR_C6; 3.
R PODOM; PF00071; TNFR C6; 3.
R PROSITE; PS00622; TNFR; 3.
R PROSITE; PS00622; TNFR NGFR 1; 2.
R PROSITE; PS0062; TNFR NGFR 1; 2.
R PROSITE; PS0062; TNFR NGFR 2; 3.
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"The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping."; Genomics 30:312-319(1995).
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CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.8%; Score 265.5; DB 1; Length 415; 30.9%; Pred. No. 5.6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; Indels
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29B326A566AEF661 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Browning J.L., Ware C.F.;
"Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 65
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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11-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last nonotation update)
15-JUN and a sequence factor receptor superfamily member 3 precursor humor necrosis factor receptor superfamily member 3
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MEDLINE-96163885; PubMed-8586432;
Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
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MEDLINE=96072804; PubMed=7594541;
Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
                              TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 21.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 RGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSST 221
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                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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TNFR-CYS 4.
TNFR-CYS 4.
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[2]
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LTBR OR TNFRSF3 OR TNFCR.
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SEQUENCE FROM N.A.
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Gaps

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225

AILLSLVLFLLFTTVLACAWMRHPSLCRKLGTLLK--RHPEGEESPPCPAPRA 275

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CRMB VARV STAN
P34015; Q89098; Q89
01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
15-JUN-2002 (Rel. 4
                            This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      "DNA sequence analysis as a criterion for allocation of the orthopoxviruses to a particular species.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute the modification of TNF-mediated antiviral processes (By
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20107289; PubMed=10639322;
Shchelkunov S.N., Totmenin A.V., Loparev V.N.,
Gutorov V.V., Chizhikov V.E., Knight J.C., Par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Garcia-1966, and Somalia-1977;
Massung R.F., Loparev V.N., Knight J.C., Ortmenin A.V., Shchelkunov S.N., Esposito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter C.J.; "Potential virulence determinants in terminal regions of variola "Botential virus genome."; smallpox virus genome."; Nature 366:748-751(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R., Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V. Kenianov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=India-1967 / Isolate Ind3;
MEDLINE=93202281; PubMede8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variola and vaccinia viruses necessary to
protective mechanisms.";
FEBS Lett. 319:80-83(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRMB
                                                                                                                                                                                                                                                                                    STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977 Loparev V.N., Parsons J.M., Esposito J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Garcia-1966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bangladesh-1975;
MEDLINE=94088747; PubMed=8264798;
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STRAIN=India-1967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  'Alastrim smallpox variola minor virus genome DNA sequences.";
                                                                                                                                                         similarity).
SUBCELLULAR LOCATION: SIMILARITY: CONTAINS 2
   .X69198; CAA49137.1;
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(Rel. 41, Last annotation update)
receptor II precursor (cytokine response modifying protein
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Q85407; Q89118;
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2 TNFR-CYS REPEATS.
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                                              (See http://www.isb-sib.ch/announce/
                                                                                        There are no restrictions
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EMBL; U88148; AAB94377
EMBL; U88149; AAB94377
EMBL; U88152; AAB94377
EMBL; U88152; AAB94377
EMBL; D36858; D36858.
PIR; S35987; S35987.
PIR; S45888; S46888.
HSSP; O14763; 1D0G.
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EMBL;
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Pfam; PF00020; TNFR_c6; 2.
ProDom; PD0000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 2.
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                                                                                                                    GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG
                                                                                                                                     VLCGEREEEARACHATHNRACRCRTGFF----AHAGFCLEHASCPPGAGVIAPGTPSQ
                                                                                                                                                       PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN
                                                                                                                                                                       PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN
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PS50050; TNFR_NGFR_
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AAA69033.1;
AAA69407.1;
AAA69467.1;
CAB54798.1;
AAB94377.1;
AAB94377.1;
AAB94377.1;
AAB94377.1;
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32.2%;
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CHARLE GLCNAC.
N-LINKED GLCNAC.
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Pred. No. 1.3e
26; Mismatches
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E -> K (IN STI
A -> E (IN STI
N -> D (IN STI
GARCIA-1966).
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GARCIA-1966)
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ND SOMALIA-1977).
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(IN STRAIN SOMALIA-1977)
(IN STRAINS BUTLER-1952
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(POTENTIAL).
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STANDARD;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Soluble TNF receptor II precursor (cytokine response modifying protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Brighton red;
PubMed=8091665;
Hu F.Q., Smith C.A., Pickup D.J.;
Hu F.Q., Smith C.A., Pickup D.J.;
Ecompox virus contains two copies of an early gene encoding a soluble secreted form of the type II TNF receptor.";
Virology 204:343-356(1994).
-!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to the modification of TNF-mediated antiviral processes.
-!- SUBCELBULAR LOCATION: Secreted.
-!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=GRI-90 / Grishak;
MEDLLINE=98229462; PubMed=9568042;
MEDLLINE=98229462; DubMed=9568042;
Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
Ryazankina O.I., Gutorov V.V., Kotwal G.J.; and right species-specific "The genomic sequence analysis of the left and right species-specific terminal region of a cowpox virus strain reveals unique sequences and a cluster of intact ORFs for immunomodulatory and host range
                       102 TTHNRICECSPGYYCILKGSSGCKACVSQTKCGIGYGV-SGHTSAGDVICSPCGLGTYSR 160
 ATHNRACRCRTGFF-----AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA 131
                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 TVSSADKCEPVPSNTFNYIDVEINLYPVNDTSCTRTTTTGISESISTSE 209
                                                                                                                                                                                                          351 AA.
                                                                                                                                                                                                                                                                                                                                      (CRMB1 OR D2L) AND (CRMB2 OR H4R).
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                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                 Orthopoxvirus.
NCBI_TaxID=10243;
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CRMB_COWPX
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amnotation update)
5-JUN-2002 (Rel. 41, Last amnotation cytokine response modifying protein
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                                                                                                                                                                                                                                               STRAIN=CMS;
PubMed=11907336;
Gubser C., Smith G.L.;
Gubser C., Smith G.L.;
"The sequence of camelpox virus shows it is most closely related to variola virus, the cause of smallpox.";
J. Gen. Virol. B3:855-872(2002).
                                                                                                              Camelpox virus (strain CMS), and Camelpox virus (strain M-96). Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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SOLUBLE TNF RECEPTOR II.
TUFF-CYS 1.
TWFR-CYS 2.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                             (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).
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                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=M-96;
Afonso C.L., Tulman B.R., Lu Z., Zsak L., Zaitsev V.L.,
Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;
Whe genome of camelpox virus.",
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribe modification of TNF-andiated antiviral processes (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EA412AF991E087F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
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EMBL; AY009089; AAG37718.1; --
EMBL; AF438165; AAL73920.1; --
INTEXPO; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6.
SMART; SM00208; TNFR; 3.
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NCBI_TaxID=203172, 203173;
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Best Local S
Matches 55
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                                                                                                                                                                                                                                             Zhang W.,
Submitted
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDIJINE=97306336; PubMed=9162061;

Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., K

Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D.,

Porter T.G., Truneh A., Young P.R.;

"A newly identified member of the tumor necrosis
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SEQUENCE
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"Herpes simplex virus-1 entry into cells
the TNF/NGF receptor family.";
Cell 87:427-436(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                     SEQUENCE FROM TISSUE=Skin;
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J. Biol. Ch
                                                                                                                                                                                                                                                                                                                                                                 superfamily with a wide tissue distribution
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TISSUE=Cervical adenocarcinoma;
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                                                                                                  Nectin-1,
                                                                                                                                          Spear P.G
                                                                                                                                                             Struyf F., Posavad
                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                Search for polymorphisms Vectin-1, and Nectin-2 in
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Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.
Eisenberg R.J., Willey D.C.;
"Herpes simplex virus glycoprotein D bound to the human receptor
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U81232;
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AAD00505.1; -.
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TNFR_NGFR_2; 2.
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TNFR-CYS 3.
Score 244; DB 1;
Pred. No. 1.8e-12
4; Mismatches 6
                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14.
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46CE13C2C70242C1
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Nat. Genet. 24:45-48(2000).
-!- FUNCTION: Receptor of the Tribility of the regulation of interactions between T-cells and dendritic cells.
-!- SUBSCELLULAR LOCATION: Type I membrane protein (Potential).
-!- ITSSUE SPECIFICITY: UBLOUITOUS EXPRESSION WITH HIGH LEVELS IN SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
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                                                                                                                                                 HATHNRACRCRIGFFA-----HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFS 130
                                                                                                                                                                                           "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
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Morinaga T., Higashio K.;
Morinaga T., Higashio K.;
differentiation factor in osteolastogenesis.";
Biochem. Biophys. Res. Commun. 253:395-400(1998).
                                                     CPKCSPGYRVKBACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLR--ASRNC
CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLER---CRYCNVLCGEREEBARAC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-UMOR necrosis factor receptor superfamily member 11A precursor (Receptor activator of NP-KB) (Osteoclast differentiation factor
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MEDINTE=9803277; PubMed=9367155;
Anderson D.M., Marskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 HATHNRACRCRTGFF--AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 CNKCEPGKYMSSKCTTTSDSVCLPCGPDEYLDSWNEEDKCLLHKVCDT--GKALVAVVAG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 NSTTPRRCACTAGYHWSQDCECCRRNTECAPGLGAQHPLQLNKDTVCKPCLAGYFSDAFS 164
                                                                                                                                                                                                                                                        Sprant Stransmembrane; Glycoprotein; Repeat; Signal; Polymorphism; Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                              FURECLES 4.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).
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AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL. SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 235.5; DB 1; Length 616;
                                                                                                                                                                                                                                                                                                                        TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11A.
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L -> LALLLLCALL (IN PDB2).
/FTId=VAR 011516.
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E3DE9A7A08196F81 CRC64;
                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
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TNFR-CYS 3.
TNFR-CYS 4.
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                                                                                                                                     EMBL; AF018253; AAB86809.1; -.
                                                                                                                                                                                                            InterPro; IPR001368; TNFR_c6.
Pfam; PF000020; TNFR_c6; 4.
Probom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66033 MW;
                                                                                                                                                HSSP; P25942; ICDF.
Genew; HGNC:11908; TNFRSF11A.
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-DB=1Esued_Patents_NA_QFWT=fastap_SUFFIX=p2n_rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51ts -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-NO XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMEOUT=120
-MARM_TIMEOUT=30 -THREADS=1 -XGAPOPT_0 - XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Perfect score:
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Maximum Match 100%
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Match Length
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1: /cgn2_6/ptcdata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptcdata/2/ina/BTUS_COMB.seq:*

6: /cgn2_6/ptcdata/2/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 7, Appli
Sequence 5, Appli
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Sequence 10, Appl	11. App	3, Appl	5, Appl	: 3, Appl	: 5, App	ω	7, App	1, Appl	; 7, App	1, App	7, Appl	1, Appl	3, Appl	3, Appl	<u>, , , , , , , , , , , , , , , , , , , </u>	: 2, Appl	. 539576	۳	1, Appl	3, Appl	125, Ap		equence 3, Appl	equence 3, Appl	quence 3, Appl	equence 3,	equence 123, Ap	equence 1, Appl	equence 1,	e 1, Appl	equence 1, Appl

## ALIGNMENTS

RESULT

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US-08-794-796-1
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                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tan, KB
APPLICANT: Truneh, Alem
APPLICANT: Young, Peter
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Tumo
                                                                                                                                                                                                                    COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                          STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 04-FE
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                                                                                                                                                                                                                                                                                                                     TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis
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271
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                                                                                                                                        Conservative:
Mismatches:
Indels:
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                                                                                                                      Length:
Matches:
                                                                                                                                                                    Gaps:
                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 1164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: CDNA
US-08-794-796-1
                                                                                                                   1,25e-109
1491.00
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TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
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Patent No. 6297367
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NEW MEMBERS OF THE AND THER FAMILIES
FILE REFERENCE: 1408.03/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapien
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Pred. No.:
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US-09-286-529-18
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US-09-286-529-18
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Sequence 19, Application US/09286529
Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF THE AND TN
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION UMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
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TYPE: DNA
ORGANISM: Homo sapien
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ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
                                         CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln
                                                                             AACCGTGCCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
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GlnAlaLeuArgValAlaArgMetProGlyLeuGluArgSerValArgGluArgPheLe	uArgArgArgLeuThrGluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuLe 	uAlaProcluGlyTrpGlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLyBLe 	DEFINE VALAN ARTHEOTHAS DITESET I TEMPENAT GLEGOSTIAT GLEGOSTICA GGCCCTCG.  CTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGCTGCTGCAGGCCCTCG.	GGACCGCTGCCTCCCCACCCCACTGCAGGAGCTGAGGAG	GlyAlaGluGluCysGluArgAlaVallleAs	AGTGGGGCCCAGAAAGCAGGGTACCTGGCAGCCCCCGCCAGTGTGTGT		GCACTGCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTCTC		TAGGCCTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCTTCTCCAGTCCCCATCGTT		GCCCTTGCCTGGGCCCCTTGCCTCTTGCAGCCAAGGTCCGAGTGGCCGCTCCTGCCCCC		GTCAGGTCCGGTCCATCTGCAGGTCCCAACTCGCCCCTTCC		GAGGCCCAATGTTAACCACTGTTGAGAAGTCACAGGGGGAAGTGA		ATGGTAATTCTCCTAACTGCCTGAGAGGAAGGTGGCCTGCCT		TCTCCTAACTGCCCGAGGGGAAGGTGGCTGGCTCCTCTGAC		ATTTGGATCTGAGCCAGGGCACAGCCTCCCCTGGAGAGCT		\GGGGTCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGC		gcacgtgcatctagcctgaggcatgccagctggctctgggaaggggccacagtggatttg		GAGGCCTGAGGGGGCAGCACACTGCAGGCCAGGCCCACTTGTGCCCTCACTCCTGCCCCT		GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCA	spThrLeuCysThrSerCysThrGlyPheProLeuSerTh	
SerValArgGluArgPheLe 268	AlaLeuLeuValArgLeuLe 248                       GCTGCTGGTGCGGCTGCT 1664	AlaAlaLeuGlnLeuLysLe 228                    CGGCCTTGCAGCTGAAGCT 1604	L	<u>س</u> و ر	CysGluArgAlaValIleAs 188	STGTGTGTGGGTGAAATGAT 1424	177	TCTCTCCTGCAAACCCCCCG 1364	177	CTTCTCCAGTCCCCATCGTT 1304	177	GAGTGGCCGCTCCTGCCCCC 1244	177	CGCCCCTTCCGATGGCCCAGGAGCCCCAA 1184	177	AGTGACCCCCTTAACATCAA 1124	177	CTCCTCTGACATGGGGAAACC 1064	177	CACGGGGAAACCGAGGCCTG 1004	177	TCTGGGAAAGTGGGCAGCAA 944	177	CCCACCAAGTCTGCCCTCTCAGGGGTGGCTGAG 884	177	AAGGGGCCACAGTGGATTTG 824		GIGCCCTCACTCCTGCCCCT 764	177		hrArgValPro 177	

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                                                                                                                  Sequence 7, Application US/09286529; Sequence 7, Application US/09286529; Patent No. 6297367; GENERAL INFORMATION:
APPLICANT: Catherine Tribouley; TITLE OF INVENTION: NEW MEMBERS OF TWF AND TNF; FILE REPRENCE: 1408.003/200130.439C1; CURRENT APPLICATION NUMBER: US/09/286,529; CURRENT FILING DATE: 1999-04-05; NUMBER OF SEQ ID NOS: 25; SOFTMARE: FastSEQ for Windows Version 3.0; SEQ ID NO 7
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Patent No. 6015938
GENERAL INFORMATION: APPLICANT: Boyle, Willaim J. APPLICANT: Lacey, David L.
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56.41%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: human
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                                                                                                                                                                                                                                                                                                 LENGTH: 459
                                                                                                          US-09-286-529-7
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US-08-974-022-5
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77
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74
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONFURER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                    E: Amgen Inc.
1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Winter, Robert B.
REFREENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEGUENCE CHARACTERISTICS:
LENGTH: 1355 base pairs
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440.50
57.75%
41.18%
29.54%
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                      CITY: Thousand Oaks
STATE: California
COUNTRY: USA
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Best Local Similarity:
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US-08-974-022-5
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US-08-795-445A-5
                                                         US-09-936-024-1 (1-271) x US-08-795-445A-5 (1-1355)
                                                                                                       Best Local Similarity:
Query Match:
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                                                                                                                                     Percent Similarity:
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APPLICANT: Boyle,
APPLICANT: Lacey,
                                                                                                                                                                                                                                                                                                                                                     NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
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NAME: Winter, Robert B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
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                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                      5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro
                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                      1355 base pairs
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Chang, Ming-Shi
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                                                                                                                                                    Length:
Matches:
                                                                                                       Mismatches:
Indels:
                                                                                         Gaps:
                                                                                                                                     Conservative:
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US-08-795-447A-5
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                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: 1)
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Boyle,
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
           TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                           FILING DATE:
                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                          STATE:
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                                           LENGTH:
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Conservative:
Mismatches:
Indels:
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Sequence 5, Application US/08974186
Patent No. 628470;
GENERAL INFORMATION:
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
ITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
COUNTRY: USA
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Best Local Similarity:
Query Match:
MOLECULE TYPE:
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NAME/KEY:

LOCATION:
US-08-795-447A-5
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Mismatches:
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Matches:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
RREFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCY ???
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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STRANDEDNESS: single
65 LeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
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STATE: California
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                                                                  ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
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APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Fran
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PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
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SOFTWARE: PatentIn versio
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OTHER INFORMATION:
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                                      CCTGGTACCTAAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGC
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US-08-974-022-1
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TITLE OF INVENTION: BHAANCED SOLUBILITY OF RECOMBINANT PROTEINS
FILE REFERENCE: A-496
CURRENT APPLICATION NUMBER: US/08/997,918
CURRENT FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PATENTIN VEY: 2.1
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Patent No. 6077689
GENERAL INFORMATION:
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LENGTH: 525
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ProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGlnProHisArgAsn
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196 GTTTGCAAGGAGCTGCAGTACGTTAAACAGGAATGCAAACCGTACGAGTATGC
                                                                                            ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro
                                                                                                                                           256 GAATGCAAAGAAGCTCGTTACCTGGAGATCGAATTCTGCCTGAAACACCGTTCCTGTCCG
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Matches:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
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APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTECERIN
NUMBER OF SEQUENCES: 53
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GASSIFICATION:
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1840 Dehavilland Drive
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APPLICATION NUMBER: 08/577,788
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Patent No. 6015938
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REPERBYCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2412 base pairs
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ADDRESSE: Amgen Inc.
STREET: 1840 Dehavillo
CITY: Thousand Oaks
STATE: California
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-795-445A-1
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                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08795445A Patent No. 6284485
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                           APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
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1840 Dehavilland
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
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APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
WUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1840 Dehavilland Drive CITY: Thousand Oaks STATE: California
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APPLICATION NUMBER: 08/577,788
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CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGRAT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/POCKET UNBER: A-378D2
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Conservative:
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APPLICANT: Lacey, David L.
APPLICANT: Lacey, David L.
APPLICANT: Clang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91362-1789
                                                                                                                       Sequence 1, Application US/08795447A Patent No. 6284728
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STRANDEDNESS: single
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Search completed: January Job time : 55 secs
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=45 -DCCALICN=200 -THR SCORE=pct -THR MX=100
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-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG-DEV TIMEOUT=10 -WARN TIMEOUT=30 -THREADS=1 -XCAPOF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR TILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR APPLICATION NUMBER: 60/164,371
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR APPLICATION NUMBER: 60/146,371
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PRIOR APPLICATION NUMBER: 60/131,964
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/131,270

FILING DATE:
APPLICATION 1

1999-04-27

RESULT 1 US-09-935-727 ; Sequence 32 ; Patent No. ; GENERAL INE ; APPLICANT: ; TITLE OF I ; FILE REFER ; CURRENT FI		45	4.4	43	4 4 2 2	40	39	یا در - ۵۵	. G	<b>3</b> 5	34	ω i	ω u N F	ب د د	2 29	28	27	200	2 C 4 R	2 2	22	21	20	18	17	16	15	145	12	1 1	10		89	7	o (	சு
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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Matches:
Conservative:
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Indels:
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PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1990-03-04
PRIOR PRIOR APPLICATION NUMBER: 09/006,352
PRIOR PLING DATE: 1998-01-13
PRIOR PLING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE PATENTIN VET: 2.1
SEQ ID NO 32
LENGTH: 903
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Best Local Similarity:
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APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: TUNAS, DANIEL B
APPLICANT: TUNAS, DANIEL B
APPLICANT: TUNAS, DANIEL B
APPLICANT: HOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POLYPEPTIGE, A TNFR HON
TITLE OF INVENTION: DCR3 POLYPEPTIGE, A TNFR HON
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
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No. US20020061559A1
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ORGANISM: Homo sal
FEATURE:
NAME/KEY: Unsure
LOCATION: 1090
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ArgSerValArgGluArgPheLeuProValHis
                                      GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu
                                                                                        ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp
                                                                                                                             GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly
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                                                                            CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGGCGCAGGAC
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                                                                                                                                                                                                                                                                                                                       ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp
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   CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln
                         TGCCAGCCGTCCCCCCAGGCACCTTCTCAGCCAGCTCCAGCTCAGAGCAGTGCCAG
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Sequence 18, Application US/09877156
Fatent No. US20020055625A1
Fatent No. US20020055625A1
Fatent No. US20020056525A1
FAPLICANT: Catherine Tribouley
FILE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT PAPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
FRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapien
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Best Local Similarity:
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                                                                                                                                        APPLICANT: ANTENNAI.

APPLICANT: BOTSTEIN, DAVID

APPLICANT: BOTSTEIN, DAVID

APPLICANT: BOTSTEIN, DAVID

APPLICANT: GURREY, AUSTIN I.

APPLICANT: GURREY, AUGTIN I.

APPLICANT: LAWRENCE, DAVID A.

APPLICANT: LAWRENCE, DAVID A.

APPLICANT: ROY, MARGARET A

APPLICANT: ROY, MARGARET A

APPLICANT: ROY, MARGARET A

APPLICANT: BOY, MARGARET A

APPLICANT: BOY, MARGARET A

APPLICANT: BOY, MARGARET A

APPLICANT: WOOD, WILLIAM I.

TITLE OF INVENTION: DCR3 POlypeptide, A TNFR Homolog

FILE REFERENCE: P1134R2 REVISED

CURRENT APPLICATION NUMBER: US/09/894,924

CURRENT FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR APPLICATION NUMBER: US 60/059,288

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: US 60/059,640

PRIOR APPLICATION NUMBER: US 60/094,640

PRIOR APPLICATION NUMBER: US 60/094,640
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Matches:
Conservative:
Mismatches:
Indels:
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968 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1000
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                                                                                         Sequence 2, Application US/09894924
Patent No. US20020065210Al
GENERAL INFORMATION:
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COCATION: 1090

JCHER INFORMATION: Unknown base

US-09-894-924-2
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGTH: 1114
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FILE REFERENCE: PF454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2001-07-06
PRIOR PPLICATION NUMBER: 60/252,131
PRIOR PPLICATION NUMBER: 60/252,131
PRIOR APPLICATION NUMBER: 60/252,598
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR PILING DATE: 2000-08-25
PRIOR PILING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR PILING DATE: 1999-08-02
PRIOR PILING DATE: 1999-08-02
PRIOR PILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR PILING DATE: 1999-04-37
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
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US-09-935-727-33
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TITLE OF INVENTION: Tumor Necrosis Factor
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; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1998-01-13
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SOFTWARE: PatentIn Ver. 2.1
; SOFTWARE: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Codon optimized TNF
US-09-935-727-33
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                                    AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr
ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp
                                                                                             GAATGTGAAAGAGCTGTTATTGATTTGTTGCTTTTCAAGATATTTCTATTAAGAGACTG
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CORGANISM: Homo sapien
US-09-877-156-19
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          186 GTGGCAGAAACACCCACCTACCCCTGGCGGACGCAGAGACAGGGGAGCGGCTGGTGC 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 GCCCAGGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCGAGACAGCCCCATGACG 305
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                                                                                                                       Sequence 1, Application US/09840795;
Patent No. US20020143147A1
GENERAL INFORMATION:
APPLICANT: Mattson, Jeanine D.
APPLICANT: Bates, Blizabeth Esther Mary
APPLICANT: Bates, Blizabeth Esther Mary
APPLICANT: Bates, Blizabeth Sther Mary
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Genes; Related Reagents
FILE REFERENCE: SF0818K
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR APPLICATION NUMBER: 09/351,777
SEQ ID NO 1
SEQ ID NO 1
LENGTH 1137
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268
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Matches:
Conservative:
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Indels:
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                                                                      261 ArgSerValArgGluArgPheLeuProValHis
                                                                                                                                                                                                                                                                                                                                               TITE: CONGANISM: primate
FEATURE:
NAME/KRY: CDS
JOCATION: (99)..(998)
NAME/KRY: misc feature
LOCATION: (1367)
OTHER INFORMATION: W; may be A or T
NAME/KRY: mat peptide
LOCATION: (132)..(998)
US-09-840-795-1
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1469.00
98.89%
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Best Local Similarity:
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                                                                                                                  US-09-840-795-1
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                CCCCACCGCAACTGCACGGCCCTGGGCCTCAATGTGCCAGGCTCTTCCTCCCAT
                                                                                                                                                                                                             GACACCCTGTGCACCAGCTGCACTGCCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG
                                                                                                                                                                                                                                                                                                      GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG
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CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln
                                                                                        ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis
                                                                                                                                                                                   AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu
                                                                                                                                                                                                                                                                           GluCysGluArgAlaVallleAspPheValAlaPheGlnAspIleSerIleLysArgLeu
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/09877156
Patent No. US20020055625A1
GENERAL INFORMATION:
TATLE OF INVENTION: NEW MEMBERS OF TNF AND TNF;
FILE REFERENCE: 1408.003/200130.43977,156
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT PILING DATE: 2001.06-08
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          966 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 998
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177	177 1	¥
1364	305 GCACTGCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTCTC	ъ 1:
177	177 ]	¥
1304	1245 TAGGCCTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCTTCTCCCAGTCCCCATCGTT 1	ъ 1:
177	177 1	¥
1244	1185 GCCCTTGCCTGGGCCCCCTTGCCTCTTGCAGCCAAGGTCCGAGTGGCCGCTCCTGCCCCC 1	ъ
177	177 1	₹
1184	1125 GTCAGGTCCGGTCCATCTGCAGGTCCCAACTCGCCCCTTCCGATGGCCCAGGAGCCCCAA 1	ъ
177	177 1	¥
1124	065 GAGGCCCAATGTTAACCACTGTTGAGAAGTCACAGGGGGAAGTGACCCCCCTTAACATCAA	ъ
177	177 ]	¥
1064	1005 ATGGTAATTCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCTCTGACATGGGGAAACC 1	ъ
177	177	¥
1004	945 TCTCCTAACTGCCCGAGGGGAAGGTGGCTGGCTCCTCTGACACGGGGAAACCGAGGCCTG	Ĕ 
177	177	ž
944	885 AATTTGGATCTGAGCCAGGGCACAGCCTCCCCTGGAGAGCTCTGGGAAAGTGGGCAGCAA	ğ
177	177	¥
884	825 AGGGGTCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGCCCCTCTCAGGGGTGGCTGAG	ğ
177	177	¥
824	765 GCACGTGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGGAAGGGGCCACAGTGGATTTG	8
177	177	¥
764	705 GAGGCCTGAGGGGGCACACTGCAGGCCAGGCCCACTTGTGCCCCTCACTCCTGCCCCT	ğ
177	177	ş
704	ACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCA	ğ
177	pThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValPro	Ş
160	141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis:	8 8
140 584	121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln	8 8
524	ATCGTGTCCACCTGGTGCCGGGGTGATTGCCCCGGGCACCCCCAGCCAG	ğ
120	CysProProGlyAlaGlyVallleAlaProGlyThrProSerGlnAsnThrGln	¥
100 464	81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis:	8 8
80	61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis	8 8
344		8

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; FEATURE:
; NAME/KEY: intron
; LOCATION: 425-560
; NAME/KEY: intron
; LOCATION: 756-1512
US-09-935-727-28
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US-09-935-727-28
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR PRICATION NUMBER: 60/252,131
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-09-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 1000-03-03
PRIOR APPLICATION NUMBER: 60/146,371
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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
FILE REFERENCE: PF454P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/09935727 Patent No. US20020150583A1
                                                                                                   LENGTH: 1796
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                        DR FILING DATE: 1999-04-30
DR APPLICATION NUMBER: 60/131,270
DR FILING DATE: 1999-04-27
DR APPLICATION NUMBER: 60/124,092
DR FILING DATE: 1999-03-12
DR APPLICATION NUMBER: 60/121,774
DR FILING DATE: 1999-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-08-02
APPLICATION NUMBER: 60/131,964
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e-90 Length: 1796 :50 Matches: 271 4% Conservative: 0 4% Mismatches: 0 5% Indea: 299 5% Gaps: 2	-09-935-727-28 (1-1796)	rpArgAspAlaGluThrGlyGluArgLeuValCys 20	GGCGGGACGCAGAGACAGGGGAGCGGCTGGTGC 1	ThrPheValGlnArgProCysArgArgAspSerProThrThr 40 	gCysAr		TyrcysAsnValleuCysGlyGluArgGluGluGluAlaArgAlacysHisAlaThrHis 80	AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100	cócaccedetretrescacacacterretresades 387	_	44		GCCCCCAGGAGTGGTGGGGGGGGGGGGGGTCAGGTTGCTGGTCCCAGCCTTGCA 507	GlyThrPr 115	GTTCCCCTGACCCTGTTCTTCCCTCCTGGCTGCAĠĆĀĊĊĊĊ 567	oSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSe 135 	15	00	7	_	9ValPro	, ,	ACGTGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGGAAGG	177	CAGTGGATTTGAGGGGTCACGCCTCCACTAGATCCCCAAGTCTGCCCT 927	117	CTCAGGGGTGGCTGAGAATTTGGATCTGAGCCAGGGCACAGCCTCCCCTGGGGAGCTCTG 987	177	GGAAAGTGGGCAGCAATCTCCTAACTGCCCGAGGGGAAGGTGGCTGGC
Scores: 2.85e-90 1287.50 imilarity: 47.54 1 Similarity: 47.54 ch: 10 35	-60	ValAlaGluThrProThrTyrProT	stegcagaadokocokoctaco	AlaGInCysProProGlyThrPheValGInArgProCy. 	CysGlyProCysProProArgHi	ITTECCCCGTGTCCACCGCGCCA	TyrCysAsnValLeuCysGlyGl 	AsnArgAlaCysArgCysArgTh	AACCGTGCCTGCCGCTGCCGCAC	AlaSerCysProProGlyAlaGl	scarcarcaccreereces		sccccaggagragragccagag		CCCTGAGCTAGGACACCAGTTCC	oSerGlnAsnThrGlnCysGlnP 	rSerGluGlnCvsGlnProHisA		oGlySerSerHisAspThrL	AGGCTCTTCCTCCCATGACACCC	gValPro	1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	CCTCACTCCTGCCCTGCACGTG	-	GGCCACAGTGGATTTGAGGGGTC		CTCAGGGGTGGCTGAGAATTTGG		GGAAAGTGGGCAGCAATCTCCTA
ent No. t S oca Mat	-936-		ω	21	41	208	61	81	328	101	m	112	448	113	508	115	, w	~	LO.	α .	175	177	808	177	868	177	928	177	988
Alignmen Pred. No Score: Percent Best Loc Query Ma DB:	60-SN	δ	<del>ද</del> ු	දු පු	ò	QQ	දු පු	φ	qq	ò	엄	ò	셤	δλ	qq	\$ E	3 8	: 음	δλ	පු	જે ક	3 8	: 심	ò	qq	λõ	qq	δ	qq

ò	177	177
qq	1048	GOGAAACCGAGGCCTGATGGTAACTCTCCTAACTGCCTGAGAGGAGGAGGTGCCTCCT 1107
ò	177	177
đ	1108	CTGACATGGGGAAACCGAGGCCCAATGTTAACCACTGTTGAGAAGTCACAGGGGGAAGTG 1167
δ	177	177
q	1168	ACCCCCTTAACATCAAGTCAGGTCCGGTCCCATCTGCAGGTCCCCAACTCGCCCCTTCCGAT 1227
ò	177	177
qq	1228	GGCCCAGGAGCCCCCAAGCCCTTGCCTGGGCCCCTTGCCTCTTGCAGCCAAGGTCCGAGT 1287
ò	177	177
ΩD	1288	GGCCGCTCCTGCCCCTAGGCCTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCTTC 1347
δ	177	177
q	1348	TCCAGTCCCCCATGGTTGCACTGCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTC 1407
ò	177	177
q	1408	TCCTGCAAACCCCCCGAGTGGGGCCCCAGAAAGCAGGGTACCTGGCAGCCCCCCGCCAGTGT 1467
ò	178	GlyAlaGluGysG 183
В	1468	GGAGTG
ò	183	eSeri
a C	1528	AGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGC 1587
ò	203	euLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGlyArgAlaA 223
q	1588	TECTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC
ò	223	laLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAspGlyAlaL 243
q	1648	CCTTGCAGCTGAAGCTGGGCTGGGGGCTCACGGAGGTCCTGGGGGGGG
ò	243	LeuVal
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<i>∂</i> 5 6	263	alargGluArgPheLeuProValHis 271                        rccGTGAGCGCTTCCTGTGCAC 1793
8 D	SULT 10 209-935 Sequenc Patent Patent TITLE TITLE TITLE TITLE RUIGE PRIOR	16-727-3  16-3 Application US/09935727  10-3 US20020150583A1  10-3 US2002015058  10-3 US2002015058  10-3 US202015058  10-3 U

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DB:
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NAME/KEY: CDS
LOCATION: (73)..(582)
US-09-935-727-3
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PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOPTWARE: Patentin Ver. 2.1
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LENGTH: 1667
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys
                                                                                                                                                                                                                                                                AlaSerCysProProGlyAlaGlyValIleAlaPro-------
                                                                                                                                                                                                                                                                                                                       AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis
                                                                                                                                                                                                                                                                                                                                                                                     TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis
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rSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPr
                                                                oSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSe
                                                                                                                                                                         GCCCCCAGGAGTGGTGGCAGGTGTGGCAGGGTCAGGTTGCTGGTCCCAGCCTTGCA
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Matches:
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Mismatches:
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Gaps:
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APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TUNAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POLYPEPTIDE, A TNFR Homolog
FILE REFERENCE: P112472 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ASHKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09896096A Patent No. US20020061559A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
LENGTH: 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure LOCATION: 62, 73, 8 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Unknown organism
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                                                                                                                                                                TyrLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArg
                                                                                          AlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAla
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 GGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACC
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63 TAACTGGAGCNCTGCCGCTACTGNAACGTCTCTGNGGGGAGCGTGAGGAGGAGGCACGG 122
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Best Local Similarity:
Query Match:
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; ORGANISM: human
US-09-877-156-7
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                      134 rSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnVa
                                                                        CAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCTTGATGT
                                                                                                         154 lProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerTh
                                                                                                                                  GCCAGGCTCTTCCTCCCATGACACCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCAC
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GRUEALL INFORMATION:

APPLICANT: BOTSTEIN, DAVID

APPLICANT: DOOGE, KELLY H.

APPLICANT: DOOGE, KELLY H.

APPLICANT: GURNEY, AUSTIN L.

APPLICANT: LAWRENCE, DAVID A.

APPLICANT: LAWRENCE, DAVID A.

APPLICANT: TUNAS, DAVIEL B.

APPLICANT: WOOD, WILLIAM I.

TITLE REFERENCE: P1134R2 REVISED;

CURRENT APPLICATION NUMBER: US/09/894,924

CURRENT FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: US 60/059,288

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1998-07-30

NUMBER OF SEQ ID NOS: 18

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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Unknown organism NAMES/REY: unsure
LOCATION: 62, 73, 86, 98
OTHER INFORMATION: unknown base
                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09894924
Patent No. US20020065210A1
GENERAL INFORMATION:
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ORGANISM: Unknown
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Pred. No.:
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US-09-894-924-3
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                              GCTTGCCACGCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCT
                                                                                        GlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThr
                                                                                                                  GGTTTCTGCTTGGAGCACGCATCGTGTCCTACCTGGTGCCGGGCGTGATTGCCCCGGGCACC
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75 AlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAla
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Fatent No. US20020055625A1
GENERAL INPORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTOR: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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Mismatches:
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US-09-062-113-92
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FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORE, Ronda P.
REGISTRATION NUMBER: 44,244
REFERENCE/DOCKET NUMBER: FJN-060DV
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7100
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207508/199
                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Releas
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 17-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: E
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ZIP: 02110
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125 High St.
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SHIMA, No. US20020051969Aluyuki
YASUDA, Hisataka
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MORINAGA, Tomonori
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MOCHIZUKI, Shin'ichi
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TSUDA, Eisuke
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                                                       706 GACATTGAAAAAACAATAAAGGCATGCAAACCCAGTGACCAGATCCTGAAGCTGCTCAGT
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                        AlaLeuGlnLeuLysLeuArgArg---
                                                                                                                                                           LeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGlyArgAla
                                                                                                                                                                                             GAAAACAGCGTGCAGCGGCACATTGGACATGCTAACCTCACCTTCGAGCAGCTTCGTAGC
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; LOCATION: 1..1206
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US-09-062-113-83
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APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: No. US20020051969Alel Proteins and Methods for Producing
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
----ACCTTGAAGGGCCTAATGCACGCA 819
                                                     820 CTAAAGCACTCAAAGACGTACCACTTTCCCAAAACTGTCACTCAGAGTCTAAAGAAGACC 879
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER: Floppy disk
COMPUTER: PROPER PROPER PROPER PROPER PROPER PROPER PROPERTION PROPERTION NUMBER: US/09/062,113
FILING DATE: 17-APR-100.
                          LeuArgValAlaArgMetProGlyLeuGluArgSerValArgGlu--
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MOCHTZUKI, Shin'ichi
YANO, Kazuki
KOBAYASHI, Fumie
SHIMA, No. US20020051969Aluyuki
YASUDA, Hisataka
NAKAGAWA, No. US20020051969Aluaki
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REGISTRATION NUMBER: 44,244
REGISTRATION NUMBER: FJN-060DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                      Sequence 83, Application US/09062113
Patent No. US20020051969A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 83: SEQUENCE CHARACTERISTICS: LENGTH: 1206 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
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Length:
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Lu, J. and Witcher, D.R.
Improving stability of flint through o-linked glycosylation Patent: WO 0142463-A 2 14-JUN-2001;
ELI LILLY AND COMPANY (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 903)
Yu,K.Y., Kwon,B., Ni,J., Zhai,Y., Ebner,R. and Kwon,B.S.
A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis
J. Biol. Chem. 274 (20), 13733-13736 (1999)
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Direct Submission
Submitted (10-MAR-1999) Micro/Immunol, Indiana University, 635
Barnhill Drive, Indianapolis, IN 46202, USA
Location/Qualifiers
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Kwon, B.S. and Yu, K.Y.
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/codon_start=1
/codon_start=1
/product="tumor necrosis factor receptor homolog"
/protein_id="AAD29688.1"
/protein_id="AAD29688.1"
/db_xref="GI:4768939"
/translation="WRALEGCGLSLICIVLALPALLPVPAVRGVAETPTYPWRDAETG
                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T_lymphocyte"
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Homo sapiens M68E mRNA, alternatively spliced, complete cds.
AF217794
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1 (2028) 1 (2010) 19. Metzker, M.L., Hilliard, C.A., Liu, X., Sandig, V., Soderman, A., Galloway, S.M., Liu, Q., Austin, C.P. and Caskey, C.T.

Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
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Direct Submission

Direct Submission

Summeytown Pike, West Point, PA 19403, USA

Summeytown Pike, West Point, PA 19403, USA

Location/Qualifiers

1. 1048

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Arganism="Homo sapiens"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein id="AAF33686.1"
/db_xref="GI:6969263"
/translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
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 AACCGTGCCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
                              TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC
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Sequence 1 from
AX082868
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1 (bases 1 to 1055)
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/db_xref="GI:13184803"
/db_xref="GI:13184803"
/translation="marlegped:SLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
ERLVCAQCEPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEA
RACHATHANRACRCTGFFAHAGFCLEHASCFPGAGVIAPGTPSQNTQCQPCPPGTFSA
SSSSSEQCEPHRNCTALGLALNVPGSSSHDTLCTSCTGFFLSTRVPGAEECERAVIDF
VAFQDISIKRLQRLLQALEAPECWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
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Sequence
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Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J., Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L., Tumas,D., Watanabe,C.K. and Wood,W.I.
                                                                                                                                                                                 Patent: WO 0073452-A 3 07-DEC-2000;
Genentech, Inc. (US)
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Pred. No. 6.6e-125;
Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 6.6
Matches 813; Conservative 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1114)
Ashkenazi, A. J., Goddard, A., Gurney, A. L., Hillan, K., Napier, M. and
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Methods and compositions for inhibiting neoplastic cell growth Patent: WO 0075316-A 1 14-DEC-2000;
Genentech, Inc. (US)
Location/Qualifiers
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

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Score 813; DB 6; I
Pred. No. 6.6e-125;
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JOURNAL
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Best Local Similarity
Matches 813; Conserv
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                                         Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 1114)
Pitti, R. M., Marsters, S. A., Lawrence, D. A., Roy, M., Kischkel, F. C.,
Dowd, P., Huang, A., Donahue, C. J., Sherwood, S. W., Baldwin, D. T.,
Goddowski, P. J., Wood, W. I., Gurney, A. L., Hillan, K. J., Cohen, R. L.,
Genomic amplification of a decoy receptor for Fas ligand in lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-NOV-1998) Molecular Oncology, Genentech, 1 DNA Way,
San Francisco, CA 94080, USA
Location/Qualifiers
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Pitti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,
Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,
Goddard,A.D., Botstein,D. and Ashkenazi,A.
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/product="decoy receptor 3"
/product=in_id="AAD03056.1"
/protein_id="AAD03056.1"
/db_xref="Gi:4106878"
/translation="MRALEGPGLSLLCLVLALPALLPVDAVRGVAETPTYPWRDAETG
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RACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA
SSSSSEQCOPHRAVCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
VAPQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
LQALRVARMPGLERSVRERFLYVH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="DcR3"
/function="binds to Fas/Apo1/CD95 ligand and blocks its
activity"
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/db_xref="taxon:9606"
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101. .1003
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REMARK COMMENT	REFERENCE AUTHORS TITLE JOURNAL	RESULT 10 BC017065 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 781 Db 968	Qy 721 Db 908	Qy 661 Db 848	Qy 601 Db 788	Qy 541 Db 728	Qy 481 Db 668	Qy 421 Db 608	Qy 361 Db 548	Qy 301 Db 488	Db 428
NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MgC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DTP/Gazdar CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	Mammali 1 (bas Straush Direct Submitt Submitt Gene CC Institu	BC017065 Homo sapiens, tumor necrosis factor receptor superfamily, member 6b, decoy, clone MGC:9587 IMAGE:3886635, mRNA, complete cds. BC017065 BC017065.1 GI:16877637 MGC. Homo sapiens Homo sapiens	CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813	GGGGCGCTGCTGGTGCGGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 780	CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGCGCTCACGAGCTCCTGGGGGCGCAGGAC 720	CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC	GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600	GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCCTCAGCACCAGGGTACCAGGAGCTGAG 540	CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT 480	TGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420	GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCAG	

Clone distribution: MGC clone distribution information can be found

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AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300
               /note="unnamed protein product"
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/db_xref="taxon:9606"
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Sequence 1 from Patent W09946376.
AX017828 GI:10042431
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 22 Row: d Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14790166.
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/product="tumor necrosis factor receptor superfamily,
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                                                                                        /db_xref="LocusID:8771"
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/closue_type="Lung, carcinoma, large cell
undifferentiated."
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/organism="Homo sapiens"
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Receptor from the superfamily of int-receptors from the human lung Patent: WO 9946376-A 1 16-SEP-1999;

BASF AG (DE); KROEGER BURKHARD (DE)

Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 6.5e-125;
iive 0; Mismatches 0;
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Sequence 18
AR171895
AR171895.1
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Tribouley, C.
                                                                                                                                                              Polynucleotide encoding TNFL1
Patent: US 6297367-A 18 02-OCT-2001;
Cocation/Qualifiers
1. 1347
                                                                                                                                                                                                                                Unknown
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                                                                                                                                                                                                                       Unclassified.
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                                                                                             100.0%; Score 813; DB 6; 1 ilarity 100.0%; Pred. No. 6.3e-125; Conservative 0; Mismatches 0;
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Bai,C.
Direct Submission
Submitted (21-DEC-1999) WP26A-1000,
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1428)
Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X., Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and Caskey,C.T.
                                                                                                                Overexpression of M68/DcR3 in human independent of gene amplification ar
                                                                                                                                                                                                                                  Homo sapiens.
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Best Local Similarity 100.0%; Pred. No. 6.2e-125;
Matches 813; Conservative 0; Mismatches 0;
West Point, PA 19403, USA
                                                                       /cell_type="germ cell tumor"
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                         /organism="Homo sapiens"
/db_rref="taxon:9606"
/chromosome="20"
/map="20q13.3"
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/product="M68C"
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/product="KIAA1088 protein"
/product="KIAA1088 protein"
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/db_xref="Gala120521760"
/db_xref="Gala120521760"
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GTGKTLCLLCTTLAWREHLRDGISARKIAERAQGELPPDRALSSWGNAAAAAGDPIAC
YTDIPKIIYASATTHSQLTQVINBLRNYSYREPKVCVLGSSREQLCIPHPSWKKGSSHLQI
HLCRKVASRSCHFYNNVERSKIEDGLASPILDIEDLYKSGSKHRVCPYLSRNLKQQ
ADIIFMPYNTLLDAKSRRAHINIDLKGTVVIPDBAHNVERWCEESASFDLIPHDLASGL
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PGDDSGVYKPGSYIFELFABAQITFGTYKGCILDSLDQIIQHLAGRAGVFTNYAGLQKL
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EKSLEFWRARDLAKRWEALRULFVEPRSKGSFSETISAYYARVAAPGSTGATFLAVCR
GKASELDFSDTRGGVIVTGLEYPPREDRYKULKMOFLDENKGGGGAGGGGEM
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/clone lib="pBluescriptII SK plus"
/note="This sequence was obtained by subcloning of the DNA fragments derived from two cDNA clones (1 - 834 was derived from a RT-PCR product (Brain) and 835 - 4945 was derived from hk02589)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kikuno,R., Nagase,T., Ishikawa,K., Hirosawa,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes.
XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 6 (3), 197-205 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-207.

Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3944)

On May 9, 2002 this sequence version replaced gi:5689512.

1. -4945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI 10-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
182 CGCGCGCCCTTGCAGCTGAAGCTGCGTCGCGGCTCACGGAGCTCCTGGGGGCGCGCAGGAC 1241
                                                                                                                               1242 GGGCGCTGCTGCTGCTGCTGCTGCAGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG 1301
                                                                                   GGGGCGCTGCTGCTGCGGCTGCTGCAGGCGCTGCGCGCGTGGCCAGGATGCCCGGGCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB029011 4945 bp mRNA linear
Homo sapiens mRNA for KIAA1088 protein, partial cds.
                                                                                                                                                                                                                                                                                                     CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 1334
                                                                                                                                                                                                                                                     781 CGGAGCGTCCGTGAGCGCTTCCTCCTGTGCAC 813
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Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
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BASE COUNT
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Matches 813;
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CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC
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                                                                                                                                                                                                                                                                                                                                                 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCCACCGCAACTGCACGGCCCTGGGCCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT
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                                                                                             GGGGCGCTGCTGCTGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAG
                                                                                                                                                                                                                                                                              TGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG
                                                                                                                                                      CGCGCGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC
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LKQRSSGSPAAGDPESSLCVEYEQEPVPARQRERGLLAALEHEGRAGSPGEEQAHSC
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GRCQACWQRHLQASRWCPACHTASRKQGVMQVFWPEPHKDHEGAGGARPVAAVGVGA
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PLHAVLELPGALPLLQRPLRGA"
1 1581 c 1529 g 872 t
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Pred. No. 4.9e-125;
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JOURNAL
                                                                                      Query Match
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                                                                      Matches 812;
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                                                                                                                                                                                  COUNT
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GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACACGGGGAGCGGCTGGTGTGC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 28 Row: o Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 14790166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ggapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
Tissue Procurement: Jenes Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC0343449 1150 bp mRNA linear PRI 08-Jt
Homo sapiens, tumor necrosis factor receptor superfamily, men
6b, decoy, clone MGC:21079 IMAGE:4752507, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
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Mammalia; Eutheria;
1 (bases 1 to 1150)
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                                                                      Conservative
                                                                                                                                                                                                                          /protein_id="AAH34349.1"
/db_xref="G1:21706465"
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                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="tumor necrosis factor receptor superfamily,
member 6b, decoy"
                                                                                                                                                                                    LQALRVARMPGLERSVRERFLPVH"
382 c 348 g 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Skin, squamous
/clone_lib="NCI_CGAP_Skn4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:21079 IMAGE:4752507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Vector: pCMV-SPORT6.ccdb"
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Pred. No. 1.2e-124;
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Search completed: January 6, 2003, 14:40:26 Job time : 2682 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match	Query Match Length	DB	ID	Description
ב	813	100.0	813	20	AAZ25377	Human mFLINT #1 nu
N	813	100.0	813	21	AAA75999	DNA encoding a mat
ω	813	100.0	813	21	AAA88730	Human FAS ligand i
4	813	100.0	813	21	AAA51077	Mature human FLINT
υ	813	100.0	813	22	AAD07380	Human mature fas l
6	813	100.0	813	24	AAD27868	<ul> <li>Human mature FLINT</li> </ul>
7	813	100.0	900	20	AAZ25375	Human FLINT #1 nuc
8	813	100.0	900	21	AAA53208	Human Fas ligand i
9	813	100.0	900	21	AAA51075	Human FLINT coding

30-MAR-1998; 20-MAY-1998; 09-SEP-1998; 17-DEC-1998; 18-DEC-1998; 18-DEC-1998; 22-DEC-1998;

98US-0079856. 98US-0086074. 98US-0099643. 98US-0112577. 98US-0112703. 98US-0112933. 98US-0113407.

30-MAR-1999;

99WO-US06797

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AAC63765	AAX23419	AAA53209	ABQ55057	AAZ92404	AAD27869	AAF77696	AAF84739	AAF84738	AAF89920	AAD07385	AAA51076	AAA88731	AAZ25376	AAA51078	AAZ25378	AAX76052	AAA53801	AAC63764	AAX07226	AAH33171	AAZ09998	AAV07654	AAC91462	AAC84421	AAA77537	AAC58581	AAC58367	AAX32744	AAD33281	AAA37772	AAV39085	380	AAF62705	AAX22300	
Human soluble TNF		y Fas lic	n ovarian	encodin	FLINT	Н			Nucleotide sequenc	Human fas ligand i	Human FLINT coding	Human FAS ligand i	Human FLINT #2 nuc	mature	Human mFLINT #2 nu	n tumour	z	Human soluble TNF	tumour necr	colon		otide se	PRO212	PRO212	PRO212	PRO212	PRO212	DcR3 po	Human tumour necro	Human tumour necro	Human tumour necro	M68 TNF receptor r	NTR3 nucle	Orphan receptor (H	

## ALIGNMENTS

17-DEC-1999 AAZ25377; AAZ25377 standard; cDNA; 813 (first entry) ВÞ

Human mFLINT #1 nucleotide sequence.

Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL; apoptosis; inflammation; cancer; diabetes; acute liver failure; sepsis; hepatitis; ischaemia-associated injury; hypercoagulation; reperfusion-associated injury; aplastic anaemia; differentiation; growth; myelodysplastic syndrome; pancytopenic condition; 07-OCT-1999 WO9950413-A2 Homo sapiens myocardial ischaemia; ss.

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20-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes therapeutic applications of mature FLINT (mFLINY) for use in the treatment of acute liver failure. Mature FLINT (mFLINY), which is a member of the tumour necrosis factor receptor superfamily, is used for treating acute liver failure, inflammation of the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated with inflammation, hepaticis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercoagulation (including use with trombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder. Type I diabetees, cancer, cell damage or damage to an innocent bystander tissue that is induced by a chemotherapeutic agent or therapeutic irradiation, treating haematopoietic progenitor cells that chare been exposed to therapeutic radiation or chemotherapy, aplastic anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is also used for promoting the growth or differentiation of a haematopoietic progenitor coll or CD34+ cell and preventing damage to a cardiac myocyte resulting from abnormal myocardial ischaemia. The present sequence
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100.0%; Pred. No. 5.1e-145;
ive 0; Mismatches 0;
                               Gould KE,
J, Na S,
                             Dou S, Glasebrook AL, Gould
Kharitonenkov A, Mizrahi J, N
Wang J, Wu X, Zuckerman SH;
                                                                                                                                                                                                                 Claim 29; Fig 3; 99pp; English.
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ELI
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(ELIL ) LILLY & CO
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Matches 813; Conserv
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The present sequence encodes a mature human FAS Ligand Inhibitory brotein (FILNT). FLINT is a homologue of tumour necrosis factor receptor proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature FLINT protein is modified to produce analogues, which have greater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibrosis;
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Witcher DR;
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GACACCCTGTGCACCAGGTGCACTGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG
                                                                                                                       GAGTGTGAGCGTGCCGTCATCGACTTTGTGTTTTCCAGGACATCTCCCATCAAGAGGCTG
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                                                                                    GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG
                                                                                                                                                                                                  DNA encoding a mature human FAS Ligand Inhibitory Protein (FLINT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, FAS Ligand Inhibitory Protein, FLINT, analogue, apoptosis, tumour necrosis factor receptor, acute lung injury, pulmonary fib acute respiratory distress syndrome; ulcerative colitis, chronic obstructive pulmonary disease, crohn's disease; ss.
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Newton CM, Noblitt TW,
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P-PSDB; AAB19334.
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Best Local Sim.
Matches 813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 813 BP; 122 A; 298
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              CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 813
                                                                         GGGGCGCTGCTGCGGCTGCTGCAGGCGCTGCGCCTGGCCAGGATGCCCGGGCTGGAG
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Pred. No. 5.1e-145;
; Mismatches 0;
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Matches 813
                                                                                                                                         inhibitory protein FLINT mature protein (see AAB19705). FLINT is a tumour necrosis factor receptor homologue that binds FAS ligand, tumour necrosis factor receptor homologue that binds FAS ligand, preventing its interaction with FAS. This interaction is implicated in runaway apoptosis and inflammatory disease. FLINT also binds to LIGHT, a membrane-bound ligand, which may play a role in immune modulation and apoptosis. The invention relates to novel FLINT analogues (see also AAB19706-09) that are resistant to proteolysis by trypsin-like proteases between positions 218 and 219 of the FLINT mature protein sequence. Nucleic acids, vectors and transformed host cells for recombinant production of the analogues are claimed. FLINT cDNA is used as a template for introducing the registrant FIINT analogues are used to prevent or treat acute lung injury, acute respiratory stress syndrome, ulcerative colitis, inhibit T lymphocyte activation, and to facilitate organ
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04-AUG-1999;
20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel protease resistant FAS ligand inhibitory protein analogues resistant to in vivo or in vitro proteolysis at amino acid posit: of the mature protein, useful for treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLINT; FAS ligand inhibitory protein; human; protease resi acute lung injury; acute respiratory distress syndrome; chronic obstructive pulmonary disease; pulmonary fibrosis; ulcerative colitis; therapy; organ transpantation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human FAS ligand inhibitor
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20-DEC-1999;
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                                                                                                                  Sequence 813 BP; 122 A; 298 C;
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 95; 100pp; English.
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                                                                         Local Similarity
 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC
                  GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGGAGCGGCTGGTGTGC
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                                                          Conservative
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99US-0140073.
99US-0147071.
99US-0160524.
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Pred. No. 5.1
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                 TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC
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Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis factor receptor (TNPR) superfamily member, which binds Fasl and LIGHT and prevents Fasl-Fas interaction. Mature FLINT (WFLINT) inhibits Fasl-Fas mediated apoptotic and pro-inflammatory activity. WFLINT is useful for treating acute respiratory distress syndrome, treating or inhibiting inchming ischemic injury during organ transplantation or for organ preservation during transplantation. MFLINT can also be used to treat acute liver failure, inflammation of the liver, abnormal (hepatocyte) apoptosis, sepsis, disorders associated with inflammation, hepaticis, ischemia, hypercoagulation or reperfusion, damage to a cardiac myocyte resulting from abnormal myocardial ischaemia, Type I diabetes, cancer, damage to an innocent bystander tissue induced by a chemocharapeutic or therapeutic irradiation, aplastic anaemias, myelodysplastic syndromes and pancytopenic conditions.
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                                                                                                                                                                                                                                                                                  Use of mature FLINT for treating e.g. acute respiratory distress syndrome, ulcerative colitis or ischemic injury during organ
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100.0%; Pred. No. 5.1e-145;
tive 0; Mismatches 0; Indels
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07-DEC-1999;
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99US-0169381.
99US-0169412.
2000US-0191430.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Human mature fas ligand inhibitory protein
(FLINT)"
/note= "CDS does not include start and stop codon"
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CC (FLINT) CDNA. FLINT, a homologue of tumour necrosis factor receptor crotein (TNPR), binds fas ligand (Fash) and thereby preventing the interaction of Fash with fas. FLINT comprising O-linked or N-linked CC oligosaccharides is useful for preventing or treating acute lung injury (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis, correctly obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF), CC to facilitate organ preservation for transplantation and to inhibit T complete activation. FLINT is useful for treating and/or preventing diseases, such as rheumatoid arthritis, fibroproliferative lung disease, (HIV), ischaemia, brain trauma/injury, human immunodeficiency virus (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-host disease, cutaneous inflammation, vascular leak syndrome, thelicobacter pylori infection, goitre, atherosclerosis, insulin dependent diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease, cromer's disease, sepsis, pancreatitis, cancer, autoimmune disease such as poriasis, Down's syndrome, and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New FLINT polypeptide for treating and/or preventing acute lung injury, acute respiratory distress syndrome, ulcerative colitis, and graft-versus-host disease, comprises O-linked or N-linked oligosaccharides -
Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is human mature fas ligand inhibitory protein (FLINT) cDNA. FLINT, a homologue of tumour necrosis factor recepto
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Query Match Best Local Matches 813; Similarity Conservative 100.0%; Score 813; DB 22; 100.0%; Pred. No. 5.1e-145; 0 Mismatches 0; Indels 0 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Administering FLINT (FAS ligand inhibitory protein) or FLINT analog, useful for treating e.g. sepsis or respiratory distress syndrome, involves pulmonary administration of a therapeutic amount of the FLINT or FLINT analog
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                                                                                                                                                                                                                                                                                             FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis; organ failure; liver; kidney; pancreas; inflammatory disease; entropolit; sepsis, acute respiratory distress syndrome; acute lung injury; systemic inflammatory response syndrome; siRS; multiple organ dysfunction; MODS; human; gene; ds.
                             /product= "Mature FLINT protein"
/note= "Does not include start and stop codons"
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treating disorders related to enhanced apoptosis (e.g. organ failure in liver, kidneys and pancreas) and inflammatory diseases associated with neutrophil activation (e.g. sepsis, acute respiratory distress syndrome, acute lung injury, systemic inflammatory response syndrome (SIRS) and multiple organ dysfunction (MODS)). The method minimises the pain mature FLINT DNA.
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                                                                                                         The present invention describes therapeutic applications of mature FLINT (C (mFLINT)) for use in the treatment of acute liver failure. Mature FLINT (mFLINT), which is a member of the tumour necrosis factor receptor. Superfamily, is used for treating acute liver failure, inflammation of the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercoagulation (including use with thrombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder. Type I diabetes, cancer, cell damage or damage to an including use with that is induced by a chemotherapeutic agent or therapeutic irradiation, treating haematopoietic progenitor cells that the late been exposed to therapeutic radiation or chemotherapy, aplastic also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte resulting from abnormal myocardial ischaemia. The present sequence
                                                              Query Match
Best Local Similarity
                                                    Matches
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dui KY,
dui Y, r
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20-MAY-1998;
09-SEP-1998;
17-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-1998;
18-DEC-1998;
22-DEC-1998;
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                                                                                                       Sequence 900
                                                                                                                                                                                                                                                                                                                                                                                                                   cancer,
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P-PSDB; AAY42182.
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                          <u>س</u>
                                                                                                                                                                                                                                                                                                                                                                                                     of mature FLINT for treating acute liver failure, inflammation, cer, and diabetes - by prevention of FasL-Fas mediated apoptotic proinflammatory activity
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GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC
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Pred. No. 5.1e-145;
Mismatches 0;
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                                                                                                                                             Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune inflammation; infectious disease; ischaemia; Alzheimer's (Parkinson's disease; Crohn's disease; transplantation; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= FLINT
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99WO-US06797.
99US-0172239.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human FLINT coding sequence.
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1..87
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88..900
/*tag=
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/*tag=
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30-MAR-1999;
20-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the coding sequence of the human Fas ligand inhibitor (FLINT). The FLINT protein is involved in cell-specific apoptosis, and can be used to treat inflammatory and autoimmune diseases such as rheumatoid arthritis, inflammatory bowel disease, funding a triffercious diseases, diabetes, psoriasis and Graves' disease, confectious diseases such as HIV-induced lymphopenia, funding the paparitis B/C chronic hepatitis and cirrhosis, and H. pylori-associated ulceration, ischaemia and reperfusion conditions including acute and atherosclerosis, and Alzheimer's and parkinson's diseases, brain trauma and injury, chronic glomerulomephritis, osteoporosis, aplastic anaemia, myelodysplasia, ulcerative colitis, bown's syndrome, and multiple sclerosis. In addition, the gene and protein can be used to prevent apoptosis following organ transplantation.
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100.0%; Pred. No. 5.1e-145;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 88-91; 101pp; English.
/product= "FLINT"
/partial
/*.90
/*tag= b
91..90
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ischaemia/Re-perfusion conditions
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98US-0111580.
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Best Local Similarity
Matches 813; Conserv
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                                                                                                                  WO200034782-A1
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09-DEC-1998;
07-JAN-1999;
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                                    sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis factor receptor (TWFR) superiamily member, which binds Fasi and LIGHT and prevents Fasi-Fas interaction. Mature FLINT (mFLINT) inhibits Fasi-Fas mediated apoptotic and pro-inflammatory activity. mFLINT is useful for treating acute respiratory distress syndrome, treating or inhibiting ulcreative colitis, inhibiting ischemic injury during organ inhibiting transplantation or for organ preservation during transplantation. mFLINT can also be used to treat acute liver failure, inflammation of the liver, abnormal (hepatocyte) apoptosis, sepsis, disorders associated with inflammation, hepatitis, ischemia, hypercoagulation or reperfusion, damage to a cardiac myocyte resulting from abnormal myocardial ischaemia, Type I diabetes, cancer, damage to an innocent bystander tissue induced by a chemotherapeutic or therapeutic irradiation, aplastic anaemias, myelodysplastic syndromes and pancytopenic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 813; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Fig 1A-B; 125pp;
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GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG
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DB; AAY96596.
                                                 GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG
                                                                        GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCCTCAGCACCCAGGGTACCAGGAGCTGAG
                                                                                                                                                                              TGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG
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                                                                                                                                                                                                               TGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCCAGCTCCAGAGCAGTGCCAG
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                                                                                                                                            CCCCACCGCAACTGCACGGCCCTGGGCCTCGATGTGCCAGGCTCTTCCTCCCAT
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100.0%; Pred. No. 5.1e-145;
vative 0; Mismatches 0;
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ischemic injury during organ
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Query Match Best Local Sim Matches 813;

Local Similarity

100.0%; Score 813; DB 20; ilarity 100.0%; Pred. No. 5.1e-145; Conservative 0; Mismatches 0;

5.1e-145;

Length Indels

903;

0;

Gaps

0

Sequence

903 BP;

129

A; 324 C; 305 G; 145 T; 0 other;

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RESULT 10
AAX22300
ID AAX22300
ID AAX22300
ID AAX22300
ID AAX2230
AC AAX2
AC AAX2
AC AAX2
DT 20-M
XX Orph
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KW HUMA
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                                                    This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The protein is related to osteoprotegerin (OPG) and to tumour necrosis factor receptor (TNFR). Host cells transformed with a vector comprising the HUMAN NTR-1 nucleic acid are used for the recombinant expression of the protein. HUMAN NTR-1 proteins and antibodies immuno specific for the protein are useful for diagnosis and treatment of humans and animals, especially muscle disorders, as receptor is involved in regulation of bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful for screening for novel binding agents, and cognate ligands, which may be used to treat disorders associated with HUMAN NTR-1 imbalance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human; tumour necrosis factor receptor; muscle disorder; bone mass; scr muscle metabolism; binding agent; cognate ligand; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel orphan human receptor polypeptide and nucleic acid - diagnostic reagents and for treatment of muscle disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW95082.
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(REGE-)
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The present sequence encodes the tumour necrosis factor (TNF) receptor polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful for treating diseases such as acquired-immunodeficiency syndrome (AIDS), anemia, autoimmune diseases, cachexia, cancer, cerebral malaria, disbetes mellitus, disseminated intravascular coagulopathy, erythroid sick syndrome, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia, obesity, rejection of transplanted organs, rheumatoid arthritis, septic shock syndrome, stroke, adult respiratory distress syndrome (ARDS), tuberculosis, and a number of viral diseases. The NTR3 polypeptide is useful for identifying or developing new (ant) agonists of NTR3. It may be used as an immunogen to which antibodies may be raised. NTR3 uncleic acid molecules may be useful as hybridisation probes in diagnostic assays to test, either qualitatively or quanticatively, for the presence of an NTR3. DNA or corresponding RNA in mammalian tissue or bodily fluid
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Matches 813; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                  M68; tumour necrosis factor; TNF; programmed cell death; apoptosis; receptor; immune response; cell differentiation; ligand; cancer; bone disease; systemic lupus erthematosus; Hashimoto's thyroiditis; Grave's disease; idiopathic myxodema; autoimmune diabetes; thrombotic thrombocytopenic purpura; multiple sclerosis; liver diseases; autoimmune gastritis; ulcerative colltis; glomerulonephritis; pulmonary fibrosis; heart failure; atherosclerosis; aplastic anaemia, myelodisplastic syndromes; osteoporosis; Alzheimers disease; Parkinsons disease; stroke; myocardial infarction; human; ds.
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The M68 protein is a member of a family of proteins which have croles in immune responses, cell death, cell proliferation and stimulation of cell differentiation. M68 lacks a transmembrane domain and is a secreted factor suggesting that it functions as a natural conhibitor for its ligand. The altered expression pattern of M68 in a multitude of tissues suggests that M68 may play a role in cancer by binding to its ligand and blocking apoptotic cell death induced by such a ligand. This anti-apoptopic role of M68 suggests that modulators of M68 will be useful in treatment of apoptosis-related diseases such as various forms of cancer and various bone disorders. M68 nucleic acids and proteins are therefore useful for treating conditions involving atypical apoptosis and for identifying modulators of M68. Modulators of M68 are useful for treatment of cancer and other diseases associated with abnormal levels of apoptosis including systemic lupus erythematosus, Hashimoto's thyroiditis, Grave's disease, idiopathic myxodema, autoimmune cliver diseases, autoimmune gastritis, ulcerative colitis, glomerulonephiritis, pulmonary fibrosis, heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated human M68 nucleic acids and proteins which are part of the tumor necrosis factor receptor (TNFR) family, useful for identifying modulators that may be used to treat various diseases e.g. cancer,
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Query Match Best Local S Matches 813 Sequence 1066 BP; 178 A; 367 C; 335 G; 186 T; 0 other;

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atherosclerosis, aplastic anaemia, myelodisplastic syndromes, osteoporosis, Alzheimers disease, Parkinsons disease, stroke, myocardial infarction.

Ó 맑 Ś S 밁 δ Ś 밁 밁 á 밁 밁 밁 á á 밁 5 140 620 481 421 361 440 301 380 241 320 181 260 200 121 61 Match 100.0%; Score 813; DB 21; Local Similarity 100.0%; Pred. No. 5.1e-145; les 813; Conservative 0; Mismatches 0; ب GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCCAGAGCAGTGCCAG AACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC CCCCACCGCAACGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCCAT CCCCACCGCAACTGCACGGCCCTGGGCCCTGAATGTGCCAGGCTCTTCCTCCCAT TGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG AACCGTGCCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC TACTGCAACGTCCTCTGCGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCAC TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC TGTGGCCCGTGTCCACCGCCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCGAGACAGCCCCACGACG GCCCAGTGCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCGAGACAGCCCCCACGACG GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC Mismatches Indels 679 540 619 420 499 360 439 300 379 240 319 180 259 120 199 60

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                                                                                                                                                                                                                                                                                        Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
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                 680 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCATCAAGAGGCTG
                                                     740 CAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAGGCTGGGGTCCGACACACAAGGCGGGG
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P-PSDB; AAW63622.
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particularly of the immune system, substantially altered (whether increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta polypeptides, nucleic acids and antibodies are claimed to be useful in the diagnosis of such disorders. Mutations of the TNFR-6 alpha and TNFR-6 beta genes can also be detected. The TNFR polypeptides are also claimed to be useful for identifying ligands which may be useful
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                                                                                                                                                                                                                                                                      Length 1077;
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                                                                                                                                                                                                                       Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;
                                                                                                                                                                                                                                                                 100.0%; Score 813; DB 19;
100.0%; Pred. No. 5.1e-145;
ive 0; Mismatches 0;
                                                                                                                                                                        in the treatment of apoptosis related disorders.
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                                                                                                                                                                                                                                                                                                                     813; Conservative
                                                                                                                                                                                                                                                                                             Local Similarity
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27-APR-1999;
30-APR-1999;
02-AUG-1999;
                                          disorders associated with neovascularisation (especially ocular neovascularisation) (such as solid tumours and malignancies (e.g. prostate cancer, breast cancer and colon cancer), diabetic retinopathy and pre-maturity macular degeneration), allergies, inflammation, thyroid associated opthalmopathy tissue/cell damage, wounds, microbial and parasitic infections, bone disease (e.g. osteoporosis), atherosclerosis, pain, cardiovascular disease (e.g. stroke), neurodegenerative disorders (e.g. Alzheimer's disease), immune disorders (e.g. graft rejection), rheumatism, liver disease, autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta; ocular neovascularisation; solid tumour; malignancy; prostate cancer; breast cancer; colon cancer; diabetic retinopathy; microbial infection; pre-maturity macular degeneration; allergy; inflammation; tissue damage; pre-maturity macular degeneration; cell damage; parasitic infection; thyroid associated opthalmopathy; cell damage; parasitic infection; bone disease; osteoporosis; atherosclerosis; cardiovascular disease; neurodegenerative disorder; Alzheimer's disease; immune disorder; graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;
                                                                                                                                                                                               alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA and protein sequences can be used in the prevention, treatment and diagnosis of diseases associated with inappropriate TNFR expression. The nucleic acids, polypeptides, antibodies, agonists and antagonists against them may be used for the treatment of a range of conditions such as
                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human tumour necrosis factor receptor proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g. Alzheimer's disease, osteoporosis and graft rejection -
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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12-MAR-1999;
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Query Match

100.0%;

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Human; tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy; immune system-related disorder; inflammatory disease; immunosuppressive; bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;
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autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy; graft versus host disease; (WHD; antiinflammatory; psoriasis; arthritis; neuroprotective; antiarteriosclerotic; dermatological; asthma; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human tumour necrosis factor receptor (TNFR)-
Galpha and 6beta protein and their corresponding nucleic acids. The
invention provides screening methods for identifying agonists and
antagonists of TMFR-6alpha and 6beta activity. The invention also
provides diagnostic and therapeutic methods for detecting and treating
immune system-related disorders. The method is useful for treating or
preventing an inflammatory disease or disorder selected from bowel
disease, encephalitis, atherosclerosis and psoriasis, an autoimmune
disease or disorder selected from systemic lupus erythematosus,
arthritis, rheumatorid arthrils, multiple sclerosis, Crohn's disease,
and autoimmune encephalitis, graft versus host disease (GVHB), and an
allergy or asthma. The present sequence is human TNFR-6alpha cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecules comprising a polynucleotide encoding humar tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides useful for treating disease e.g. inflammatory and autoimmune disorders
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BQ687526 AGENCOURT
BM767535 K-EST0050
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AUTHORS
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          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11440 row: n column: 15
High quality sequence stop: 758.
Location/Qualifiers
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BI821789
BI821789.1 GI
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1118)
11 Homo: H
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603035863F1 NIH_MGC_115
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BQ7163363
BQ7163363
BM756087
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BIP18743
BM8313348
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BM738195
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AI290210
AI561219
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BF339551
AW262121
AW262121
BQ019285
BI838357
BE879166
AW471440
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BF001490 7988h10.x
AW083914 xc25g02.x
AW084771 UI-H-BI0-BM738195 K-EST0002
BM6737727 UI-E-CQ0-
AI857725 w121a08.x
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AW204999 UI-H-B11-
AA025673 Ze90h09 s
AIZ90210 q179912 x
AW771720 h171a02 x
AIT561211 tq27c11 x
BM833463 K-ESTT0108
AW769220 h154h07 x
AW316995 xx10e06 x
AW316995 xx10e06 x
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AW262121 xq31a04.x
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BE878908.1 GI:10327684
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99.8%;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Best Local Similarity 99.8
Matches 605; Conservative
                               mRNA sequence.
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                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                    source
    LOCUS
                                                                                                                                                               AUTHORS
TITLE
JOURNAL
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="INAGE:5176910"
/clone="INAGE:5176910"
/clone="INAGE:5176910"
/clone="Moge:5176910"
/clone="Morgan: pooled brain, lung, testis; Vector:
pcMv-SPORT6; Site_1: Not!; Site_2: EcoRv (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27;
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRv site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                80.8%; Score 657; DB 13; Length 1118;
.larity 99.4%; Pred. No. 2.2e-113;
Conservative 0; Mismatches 0; Indels 4.
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BE878908 617 bp mRNA linear EST 20-OCT-2000 601492609F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894794 5',
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/clone="IMAGE:3894794"
/clone=lib="NIH_MGC_69"
/clone=lib="NIH_MGC_69"
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/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not1;
Site_2: SAll; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                               Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                      1 (bases 1 to 617)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih,gov
Tissue Procurement: DCTD/DTP/Gadar
Tissue Procurement: DCTD/DTP/Gadar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9685 row: a column: 03
High quality sequence stop: 617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
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Program for Rat Gene Discovery and Mapping
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1 (bases 1 to 728)
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                                                                                                                                                         /tissue_type="fetal eye"
/dev gtage="fetal"
/lab_host="DH10B [Life Technologies] (T1 phage resistant)"
/note="Organ: eye, Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UT-E-EO1 is a normalized CDNA library containing the
following tissue(e): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Ger Discovery in the Visual System, supported by National Eye
                                                                                                                                                                                                                                                                                                                                /clone="UI-E-EO1-ajc-j-12-0-UI"
/clone_lib="UI-E-EO1"
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/db_xref="taxon:9606"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (Dases 1 to 679)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
   Email: ggapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                          mRNA sequence
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TAG_TISSUE-human fetal e
TAG_SEQ=CGCGTATACC"
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                                                                                                                                                                                                                                                                                                               IMAGE:3891908
                                                                                                                                                                                   Euteleostomi;
       (LLINI)
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698

166 758 226

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638 346 578 406 521 466 461 526 401 586 341 646 281

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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                            /organism="Homo sapiens"

/db_xref="taxon:9606"

/db_mcf="taxon:9606"

/clone=lib=NNH MGC 69"

/tissue_type="large_cell carcinoma, undifferentiated"

/lab_host="DH10B (phage-resistant)"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;

Site_2: Sall; Cloned unidirectionally. PrimeT: Oligo dr.

Average_insert_size_1: lkb. Library constructed by Life
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 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution. MGC clone distribution information can
found through the I.M.A.G.E. Consortium/Linn at:
http://image.llnl.gov
Plate: LinMa677 row: h column: 21
High quality sequence stop: 672.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                               Length 679;
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100.0%; Pred. No. 1.9e-98;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                 Technologies.
239 c
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Matches 577; Conservative
                                                                                                                1. .679
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ORIGIN
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AGENCOURT\_8345883 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6250691 5', mRNA sequence. BQ687526 BQ687526.1 GI:21812842

DEFINITION

RESULT 5 BQ687526 ACCESSION VERSION

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/organism="Homo sapiens"
/do xref="taxon:966"
/clone="IMAGE:6250691"
/clone=in="MAGE:6250691"
/clone=in="MIH MGC 110"
/tissue_type="ductal carcinoma, cell line"
/tlab_hofe="MIH MG (Plage resistant)"
/note="Organ: pancreas; Vector: pOTFD; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the Directionals, adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library " lothers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (Lases 1 to 863)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: Rubin Laboratory
CONA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLCM2394 row: c column: 12
High quallity sequence stop: 599.
Location/Qualifiers
                                   Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
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Matches 637; Conservative
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                                                                                 REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Adminalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 572)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and vim ve.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: yongsung@mail.kribb.re.kr
Plate: 3 row: E column: 03
High quality sequence stop: 572.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim, Y.S.
21C Frontier Korean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM767535.1 GI:19097150
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/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and
                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Lymphoblast-like"
/cell_line="SNU-5"
/lab_host="Top10F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Ascites"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="S1SNU5s2-3-E03"
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VERSION KEYWORDS SOURCE

ORGANISM

human.

Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

ACCESSION DEFINITION FOCUS.

BM480312 1203 bp AGENCOURT 6424187 NIH\_MGC\_67 Homo 5', mRNA sequence. BM480312 BM480312.1 GI:18529354 EST.

sapiens mRNA

CDNA linear E cDNA clone

EST 05-FEB-2002 MAGE:5491790

RESULT 7 BM480312

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                          GGGCCGCGCGCCTTGCAGCTGAAGCTGCGTC
                                                                             GCTGCAGCGGCTGCAGGCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGC
                                                                                                       GCTGCAGCGGCTGCAGGCCCCTCGAGGCCCCGGAGGGCTGGGGTCCGACACCAAGGGC
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GGGCCGCGCCTTGCAGCTGAAGCTGCGTC
                                                                                                                                                        TGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAG
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Pred. No. 1.3e
0; Mismatches
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| crganism="Homo sapiens" |
| crganism="Homo sapiens" |
| crganism="Homo sapiens" |
| clone="ITMAGE:4752507" |
| clone="ITMAGE:4752507" |
| clone="ITMAGE:4752507" |
| clone="ITMAGE:4752507" |
| clone="IDHOB (TI phage=resistant)" |
| lab host="DH10B (TI phage=resistant)" |
| note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; |
| site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. |
| Average insert size 1.5kb. Library constructed by Life |
| Technologies: Note: this is a NCI_CGAP Library." |
| Technologies: Note: this is a NCI_CGAP Library." |
                                                                                                                                                                                                                          602627514F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752507 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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733 GGAGTGTGAGCGTGCCCTCCATCCACTTTGTGGGCTTTTCCAGGACCTCTTCCTAAA 792
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Pred. No. 2e-89;
0; Mismatches 95; Indels
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85.9%;
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JOURNAL
COMMENT
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/db_xref="taxon:8606"
/db_xref="taxon:8606"
/clone="IMAGB:5491790"
/clone="IDHIDE="NH MGC 67"
/tissue type="retinoblastoma"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_I: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Liff
Technologies."
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                          In loases to 1203)
MIH-MGC hetp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone distribution: MGC clone distribution information on the found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12112 row: n column: 15
High quality sequence start: 4
High quality sequence start: 4
High quality sequence stop: 560.

Location/Qualifiers
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                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution informat:
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9508 row: p column: 04
High quality sequence stop: 701.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 874)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg,
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4186995"
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/clone_type="G_lioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: N:
                                                                                                                    1. .874
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sapiens cDNA clone
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   Site_1: NotI;
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                                                                                                                                                    AW083241
692 bp mRNA linear EST 14-OCT-1999 xc07a04.x1 NCI CGAP CO21 Homo sapiens cDNA clone IMAGE:2583534 3' similar to TR:095407 DECOY RECEPTOR 3. ;contains L1.b1 MER22 repetitive element ;, mRNA sequence.

AW083241
                        Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalla; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 692)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
           Tumor
Unpublished (1997)
                                                                                                Homo sapiens
                                                                                                                          AW083241.1
EST.
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Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Pred. No. 5.7e-84
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
similar to TR:095407 095407 DECOY RECEPTOR 3. ;contains TAR1.b1
TAR1 repetitive element ;, mRNA sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
                                                               AW262121.1 GI:6638937
                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                         /db xref="taxon:9606"
/clone="IMAGE:2583534"
/clone="IMAGE:2583534"
/clone="IMAGE:2583534"
/clone="IMAGE:2583534"
/tissue_type="moderately differentiated adenocarcinoma"
/tissue_type="moderately differentiated adenocarcinoma"
/lab host="DA10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Normalized to Cot >500. Average insert size 1.04kb.
Normalized version of NCI_CGAP_Col8. Library constructed by Life Technologies."
36 a 205 c 235 g 115 t 1 others
         Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technogies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIAL at:
Seq primer: -40UP from Gibco
High quality sequence stop: 414.
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Pred. No. 9.1e-81;
0; Mismatches 10
                                                                                                                                                                                                                                                                                       1. .692
/organism="Homo sapiens"
    Contact: Robert Strausberg, Ph.D.
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Matches 510; Conservative
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Best Local Similarity 100
Matches 458; Conservative
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                      GCCAGCCCCACCGCAACTGCACGGCCCTGGGCCCTGGCCCTCAATGTGCCAGGCTCTTTCCT
                                                                                     cGCAGTGCCAGCCGCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGT 509
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Email: cgapbs r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iow

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQ019285 568 bp mRNA linear UI-H-DT1-awn-l-19-0-UI.sl NCI_CGAP_DT1 Homo sapiens IMAGE:5891874 3', mRNA sequence.
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Unpublished (1997)
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Seq primer: M13 FORWARD
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Lung; Vector: pT773.Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; MCI CGAP DT1 is a normalized cDNA library containing the following tissue(s): Metatastic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonuclectide containing a Not I site.
                                                                                                                                                                                                                                                                                                            TAG_LIB=UI-H-DT1
TAG_TISSUE=lung metatastic chondrosarcoma
TAG_SEQ=AACTGTTCGG"

170 c 187 g 105 t
                                                                                                                                                                                                                                                                                                                                                                                                                          used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:5891874"
/clone_lib="NCI_CGAP_DT1"
/tissue_type="Metastatic Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                         library is AACTGTTCGG.
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/db_xref="taxon:9606"
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Pred. No. 3.6e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11559 row: 1 column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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1 (bases 1 to 588)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      97
               /note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH MGC Library."

224 c 171 g 95 t 1 others
                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="IMAGE:522545"
/clone="IMAGE:522545"
/clone=lib="NIH_MGC_120"
                                                                                                                                                                                                                              'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Query Match

Score 428.6;

BB 13;

Length 588;

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xw59e06.X1 NCI CGAP Panl Homo sapiens cDNA linear EST 24-FEB-2000 xw59e06.X1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2832323 3' similar to TR:095407 095407 DECOY RECEPTOR 3.;contains TAR1.bl AW471440
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Mashington University Genome Sequencing Center
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-GEPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Seq primer: -40UP from gloco
High quality sequence stop: 387.
Location/Qualifiers
             Library constructed by Life
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 540)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                        12;
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Pred. No. 2.3e-69;
         Average insert size 1.1 kb. Technologies."
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                                                                                                        51.9%;
98.7%;
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Best Local Similarity 98.7
Matches 446; Conservative
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTPF/Gazdar
Tissue Procurement: DCTD/DTPF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9670 row: I column: 01
High quality sequence stop: 546.
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/note="Organ: lung; Vector: pGWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                     CGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCGCCACTACACGCAGTTCTGG 159
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             Best Local Similarity
Matches 431; Conserv
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/clone=lib="NCI CGAP Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
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Minimum DB
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Perfect score:
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Match Length DB
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1: /cgn2_6/ptcdata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/2/ina/FTUS_COMB.seq:*
5: /cgn2_6/ptcdata/2/ina/backfiles1.seq:*
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(c) 1993 - 2003 Compugen Ltd.
                         US-08-794-796-1
US-09-286-529-18
US-09-286-529-7
US-09-286-529-7
US-08-997-918-47
US-08-997-918-47
US-08-995-445A-1
US-08-795-446B-1
US-08-795-447A-1
US-08-795-447A-3
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Sequence 19, Appl
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Sequence 14, Appl Sequence 14, Appl	Sequence 1, Appli	ω,	12	Sequence 12, Appl		Sequence 3, Appli	Sequence 10, Appl	Sequence 11, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 18, Appl	Sequence 1, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 22, Appl	Sequence 3, Appli

## ALIGNMENTS

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; TOPOLOGY: 1; MOLECULE TYPE: US-08-794-796-1
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; Patent No. 5885800
; GENERAL INFORMATION:
APPLICANT: Emery,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASUSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION UNWBER: US/08/794,796
FILING DATE: 04-FEB-1997
CLASSIFICATION UNWBER: PILING DATA:
APPLICATION NUMBER:
APPLICATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tan, KB
APPLICANT: Truneh, Alem
APPLICANT: Young, Peter
TITLE OF INVENTION: Tunor Necrosis
TITLE OF INVENTION: TR4
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                    LENGTH: 1164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STREET: 709 Swedeland
CITY: King of Prussia
STATE: PA
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ZIP: 19406
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Score 813; DB 2;
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; ORGANISM: Hon
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                                                           GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCAGACG
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Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: BW MEMBERS OF TNF AND TNF
PILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
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                   Score 813; DB 4; L
Pred. No. 2.6e-154;
Mismatches 0;
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Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TWI
FILE REFERENCE: 1408.003/200130.439C1
100.0%; scc-
100.0%; Pre
                                                                     Conservative
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1004

900

1064

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1184

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; SEQ ID NO 19
; LENCTH: 1859
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-286-529-19
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                                                                          GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF THE AND
FILE REFERENCE: 1408.03/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOPTWARE: FastSEQ for Windows Version
SEQ ID NO 7
LENGTH: 459
TYPE: DNA
ORGANISM: human
S-09-286-529-7
                                                                                                                                                                       Sequence 7, Application US/09286529
Patent No. 6297367
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Best Local Similarity
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CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.9e-98;
0; Mismatches 6
                                                                                                                                   TNFR FAMILIES
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CURRENT APPLICATION NUMBER: US/08/997,918
CURRENT FILING DATE: 1997-12-24

NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 525
TYPE: DNA
CREATION: Artificial Sequence
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Best Local (
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Snavely, Marshall TITLE OF INVENTION: ENHANCED FILE REFERENCE: A-496
                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: fragment encoding amino acids 22-194 of human
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                        GTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACG
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                                                                                                                        CACCTAAATATCTTCATTATGATGAAGAAACTAGTCACCAGCTGCTGCGGCGACAAATGTC
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Pred. No. 7.2e-18;
0; Mismatches 234;
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STRANDEDNESS:
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247;
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Matches
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           194 CGGTTTGCAAGGAGCTGCAGTACGTTAAACAGGAATGCAACCGTACGCACAACCGTGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022 FILING DATE: 12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STREET: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release.
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
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52.3%;
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
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LOCATION:
US-08-974-022-1
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Gaps
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Mismatches 225; Indels
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COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: PER PLOPPY disk
COMPUTER: PER PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
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APPLICANT: Boyle, Willaim J.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2432 base pairs
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1840 Dehavilland Drive
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US-08-795-447A-1
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Best Local Similarity
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                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boyle, William J. APPLICANT: Lacey, David L. APPLICANT: Calzone, Frank J. APPLICANT: Chang, Ming-Shi
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
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                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Osteoprotegerin NUMBER OF SEQUENCES: 53
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LOCATION:
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                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                 91362-1789
                                                                                                                                                                                                                                SSEE: Amgen Inc.
T: One Amgen Center
Thousand Oaks
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Pred. No. 2.8e-14;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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271
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                               GCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCA
                                                               GGTGAGACGTCATCGAAAGCACCCTGTAGGAAACACACCAACTGCAGCTCACTTGGCCTC
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                                                                                                                               CAGGCTGGGACCCCAGAGCGAAACACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 112; DB 4;
Pred. No. 2.8e-14;
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US-08-974-186-1
US-08-974-186
; Sequence 1, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
 APPLICANT: Boyle, Willaim J.
 APPLICANT: Lacey, David L.
 APPLICANT: Calzone, Frank J.
 APPLICANT: Chang, Ming-Shi
 TITLE OF INVENTION: OSTEOPROTEGERIN
 NUMBER OF SEQUENCES: 53
; CORRESSE: Amgen Inc.
 STREET: 1840 Dehavilland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320-1789
; COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

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52.3%; Pred. No. 2.8e-14;
tive 0; Mismatches 225; Indels
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Patent No. 6288032
GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTBOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE AMGEN INC.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILLING DATE:
CLASSIFICATION:
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STREET: 1840 Dehavilland Drive
                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          NAME: Winter, Robert B.
REPERRENCE/POCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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LENGTH: 2432 Dacc
TYPE: nucleic acid
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; LOCATION:
US-08-974-186-1
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US-08-795-446B-1
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SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
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US-08-706-945D-123
; Sequence 123, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Winter, Robert B.
REPERBENG/DOKKET NUMBER: J
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2432 base pairs
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EDNESS: single
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124..1326
  California
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                                             91320-1789
                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic
STRANDEDNESS:
                         USA
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MOLECULE TYPE:
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LOCATION:
STATE: C
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; NAME/KBY: CDS
; LOCATION: (124)..(1326)
; OTHER INFORMATION:
US-08-706-945D-123
                                                                                                                                                                                                                     RESULT 12
US-08-974-022-3
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SEQ ID NO 123
LENGTH: 2432
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Best Local Similarity 52.3%;
Matches 247; Conservative
                                                                                                                                                                              Sequence 3, Application US/08974022 Patent No. 6015938
                                                                                  GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
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APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
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                                                   TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
                              CORRESPONDENCE ADDRESS:
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 STREET:
                   ADDRESSEE:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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LENGTH: 1324 base pair
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                                                                    451
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603 CTGCTAATTCAGAAAGGAAATGCAACATGACAACGTGTGTTCCCGGAAACA
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Pred. No. 5.5e-14;
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RESULT 13 US-08-795-445A-3

Sequence 3, Application US/08795445A Patent No. 6284485 GENERAL INFORMATION:

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91 CGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCCGTGTCCACCGCGCGCACTACACG 150
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603 CTGCTAATTCAGAAAGGAAATGCAACACATGACAACGTGTGTTCCGGAAACA 654
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
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                                                                                                                                                                                       Sequence 3, Application US/08795447A
Patent No. 6284728
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ 1D NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
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US-08-795-447A-3
                                                                                                                                       RESULT 14
US-08-795-447A-3
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                                                                                                                                                                                                                                                                       STREET: 1840 Delavilland Drive
CITY: Thousand Oaks
STATE: California
CUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PAETENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
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13.6%; Score 110.4; DB 4;
Best Local Similarity 52.1%; Pred. No. 5.5e-14;
Matches 246; Conservative 0; Mismatches 226;
      APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
UNDER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                  E: Amgen Inc.
1840 Dehavilland Drive
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APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1324 base pairs
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STRANDEDNESS: single
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CLASSIFICATION:
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US-08-974-186-3
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US-08-974-186-3
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 3:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                               183
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STREET: 1840 Dehavilland
CITY: Thousand Oaks
STATE: California
COINTED. YOU
                                                                                                                                                 91
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 91320-1789
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                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                       GACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCCAGTGCCCCCCAGGCACCTTTGTGCAG 90
                                                GACAGCTGGCACACCAGTGATGAGTGTGTGTATTGCAGCCCAGTGTGCAAGGAACTGCAG
                                                                                                                                      CGGCCGTGCCGAGACACACCACGACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG 150
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                                                                               CAGTTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGCGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1324 base pairs
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                           CDS
90..1292
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                                                                                                                                                                                                                                                                          Length 1324;
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Search completed: January 6, 2003, 15:14:31 Job time : 59 secs

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Post-processing: Minimum Match 0%
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Maximum DB seq length: 200000000
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Perfect score:
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
103	103	103	103	103	103	103	103	103	103	103	103	103	103	103	103	103.4	152.2	152.2	179	183	194.2	194.2	200	200	
12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	18.7	18.7	22.0	22.5	23.9	23.9	4	4	•
1206	1206	1206	1206	1206	1206	1203	1200	1182	1089	1056	984	981	966	819	594	564	277	277	191	233	199	199	201	201	
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US-09-062-113-87	-062-113-	062-113-	US-09-062-113-84	US-09-062-113-83	US-09-062-113-6	US-10-105-934-3	US-09-062-113-94	US-09-062-113-100	US-09-062-113-10	US-09-062-113-95	US-09-062-113-93	US-09-062-113-92	US-09-062-113-101	US-09-062-113-96	US-09-062-113-97	US-09-062-113-102	US-09-894-924-7	US-09-896-096A-7	US-09-935-727-18	US-09-292-758-141	US-09-894-924-8	US-09-896-096A-8	US-09-894-924-6	US-09-896-096A-6	
Sequence 87, Appl	86,	-	84,	Sequence 83, Appl	Sequence 6, Appli	υ, Α	94,	Sequence 100, App	10,		•	92,	101,	Sequence 96, Appl	Sequence 97, Appl	Sequence 102, App	Sequence 7, Appli	Sequence 7, Appli	Sequence 18, Appl	Sequence 141, App	Sequence 8, Appli	Sequence 8, Appli	Sequence 6, Appli	Sequence 6, Appli	•

## ALIGNMENTS

RESULT 1 US-09-935-727-1

PRIOR FILING DATE: 1997-0
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 1
LENGTH: 1077
TYPE: DNA Sequence 1, Application US/09935727 Patent No. US20020150583A1 GENERAL INFORMATION: PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR APPLICATION NUMBER: 60/035,496 PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR ETIZING DATE: 1000-03-04 PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21 FILE REFERENCE: PF454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: 60/131,964 PRIOR FILING DATE: 1999-04-30 PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931 PRIOR APPLICATION NUMBER: 60/303,224 TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta APPLICANT: Human Genome Sciences, Inc PRIOR FILING DATE: 1999-08-02 PRIOR APPLICATION NUMBER: 60/227,598 ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS APPLICATION NUMBER: 60/168,235 FILING DATE: 1999-12-01 FILING DATE: 2000-03-03 APPLICATION NUMBER: 60/146,371 1997-01-14

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NAME/KEY: Unsure LOCATION: 1090
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                               Length 1077;
                                                 Indels
                            100.0%; Score 813; DB 10;
100.0%; Pred. No. 7.8e-162;
ive 0; Mismatches 0;
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Sequence 2, Application US/09896096A
Patent No. US20020061559A1
GENERAL INPORMATION:
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APPLICANT: BOTSTETN: DAVID
APPLICANT: DODGE, KELLY H
APPLICANT: GURNEY, AUSTIN L.
                                       Best Local Similarity 100. Matches 813; Conservative
LOCATION: (25)..(924)
    ; LOCATION: (
US-09-935-727-1
                               Query Match
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                 APPLICANT: LAMERNCE, DAVID A. APPLICANT: PITTI, ROBERT A APPLICANT: PITTI, ROBERT A APPLICANT: ROY, MARGARET A APPLICANT: ROY, MARGARET A APPLICANT: WOOD, WILLIAM I. TITLE OF INVENTION: DCR3 POLYDEDLIGE, A TNFR HOMOLOG TITLE OF INVENTION INCR3 POLYDEDLIGE, A TNFR HOMOLOG CURRENT APPLICATION NUMBER: US/09/896,096A CURRENT TILING DATE: 2001-06-28 PRIOR APPLICATION NUMBER: US 60/059,288 PRIOR FILING DATE: 1998-09-18 PRIOR APPLICATION NUMBER: US 60/059,288 PRIOR RILING DATE: 1998-09-18 PRIOR PRILING DATE: 1998-07-30 PRIOR FILING DATE: 1998-07-30 PRIOR FILING DATE: 1998-07-30 PRIOR FILING DATE: 1998-07-30
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100.0%; Score 813; DB 10;
Best Local Similarity 100.0%; Pred. No. 7.8e-162;
Matches 813; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Unknown base US-09-896-096A-2
KIM, KYUNG JIN
LAWRENCE, DAVID A
PITTI, ROBERT
ROY, MARGARET A
TUMAS, DANIEL B
WOOD, WILLIAM I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: ASKIKENAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: DODGE, KELLY H.
APPLICANT: KIM, KYUNG JIN
APPLICANT: KIM, KYUNG JIN
APPLICANT: ROY, MARGARET A
APPLICANT: ROY, MARGARET A
APPLICANT: TUNAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POLYPEPTIDE, A TUFR HOM
FILE REFERENCE: P1134RZ REVISED
CURRENT APPLICATION NUMBER: US/09/894,924
CURRENT APPLICATION NUMBER: US 09/157,289
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
TYPE: DNA
ORGANISM: HOMO Sapiens
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US-09-894-924-2
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Best Local Similarity
Matches 813; Conserv
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NAME/KEY: Unsure
LOCATION: 1090
OTHER INFORMATION: Unknown
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 1347
TYPE: DNA
CRGANLEM: Homo sapien
US-09-877-156-18
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                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                 Matches 813;
                                                                                                                                                                                                                                                                                                                              APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TWF AND
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
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                                                               GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCCACGACG
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                                                                                         AACCGIGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
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                                                TGCCAGCCGTGCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG
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                          GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG
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APPLICANT: Murphy, Erin E.
APPLICANT: Mattson, Jeanine D.
APPLICANT: Bates, Eliabeth Esther Mary
APPLICANT: Bates, Eliabeth Esther Mary
APPLICANT: Bates, Eliabeth M.
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Genes; Related Reagents
FILE REFERENCE: SPO0818K
CURRENT APPLICATION NUMBER: US/09/840,795
CURRENT APPLICATION NUMBER: 09/351,777
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR APPLICATION NUMBER: 09/351,777
PRIOR APPLICATION NUMBER: 09/351,777
SROOF FLING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 1
LENGTH: 1137
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Patent No. US20020143147A1
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LOCATION: (99)..(998)
NAME/KEY: misc_feature
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                                                                                                                         99.6%; Score 809.4; DB 10
99.6%; Pred. No. 4.4e-161;
iive 1; Mismatches 2;
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US-09-877-156-19
; Sequence 19, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
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Matches 810; Conservative
LOCATION: (367)
OTHER INFORMATION: W;
NAME/KEY: mat_peptide
LOCATION: (132)..(998)
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US-09-840-795-1
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US-09-935-727-32
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                                                                                                                                           Sequence 32, Application US/09935727 Patent No. US20020150583A1 GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 1859
TYPE: DNA
ORGANISM: Homo sapien
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha
FILE REFERENCE: PF454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
PRIOR RAPPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NEW MEMBERS OF TWF AND FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
NUMBER: FREESEQ for Windows Version 3.0
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Pred. No. 2.6e-103;
0; Mismatches 6;
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PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
ELECTH: 903
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Best Local S
Matches 627
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ORGANISM: Artificial Sequence
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APPLICATION NUMBER: 60/121,774
FILING DATE: 1999-03-04
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APPLICATION NUMBER: 60/131,964
FILING DATE: 1999-04-30
APPLICATION NUMBER: 60/131,270
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FILING DATE: 1999-12-01
APPLICATION NUMBER: 60/146,371
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FILING DATE: 2000-08-25
APPLICATION NUMBER: 09/518,931
FILING DATE: 2000-03-03
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APPLICATION NUMBER: 60/124,092
GAGTGCGAACGCGCTGTGATCGACTTTGTGGCCTTCCAGGATATCTCTATCAAAAGGCTG
                  GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG
                                                         GATACTCTGTGTACAAGCTGTACTGGCTTTCCTCTCTCTACCCGCGTGCCTGGCGCGCAA
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Pred. No. 1.4e-99;
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TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAAT 360
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CTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCA 240
                                                                                                                                                                                                                                                                                                                                           520 ACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGCGCTTTCCAG 579
                                                                                                                                                                                                                                                                                                                                                                                    421 ACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAG 480
                                                                                   1 GCCGAGACACCCCCACGACGTGTGGCCCGTGTCCACCGCGCCCACTACACGCAGTTCTGGA
                                                CCCCCAGCCAGAACACGCAGTGCC-AGCCGTGCCCCCAAGGCACCTTCTCAGCCAGCAGC
                                                                                                                                             400 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROY, WARGARET A
APPLICANT: TUMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/894,924
CURRENT APLLING DATE: 2001-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.2%; Score 473.4; DB 10; 98.8%; Pred. No. 7.6e-91; iive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/157, 289
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059, 288
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094, 640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
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OTHER INFORMATION: Unknown organism
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; Patent No. US20020065210Al
; GENERAL INFORMATION:
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LOCATION: 62, 73, 86, 98
OTHER INFORMATION: unknown base
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APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: IAWRENCE, DAVID A.
APPLICANT: BOY, WARGARET A
APPLICANT: TUMAS, DANIEL B
APPLICANT: TUMAS, DANIEL B
APPLICANT: TUMAS, DANIEL B
APPLICANT: TUMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 98.8
hes 485; Conservative
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                                                                 GGGGCGCTGCTGCTGCTGCTGCTGCGCGTGCCCTGGCGCTAGGATGCCCCGGGCTGGAG
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APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: COUREY, AUGTIN L.
APPLICANT: CHUREY, AUGTIN L.
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: TUMAG, DAVIEL B
APPLICANT: TOWAG, DAVIEL B
APPLICANT: TOWAG, DAVIEL B
APPLICANT: TOWOD, WILLIAM I.
TITLE OF INVENTION: DCR3 POLYPEPTIGG, A TNFR Homolog
FILE REPERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
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ilarity 98.8%; Pred. No. 7.6e-91;
Conservative 0; Mismatches 5;
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LOCATION: 62, 73, 86, 98
OTHER INFORMATION: unknown base
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Best Local Similarity
Matches 485; Conservat
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
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LENGTH: 491
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Sequence 7, Application US/09877156
Patent No. US2002005625A1
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF THE AND TN
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/877,156
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR APPLICATION NUMBER: US 09/286,529
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 459
; TYPE: DNA
; ORGANISM: human
US-09-877-156-7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      Matches 459;
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GGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCCCCTCAGCACCAGG
                                                TCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCA 465
                                                                                                                AGCCAGAACACGCAGTGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCCAGCAGCTCCCAGC
                                                                                                                                                                            TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCCGGGCACCCCC
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                                                                                             TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCC
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US-09-935-727-33
; Sequence 33, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
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US-09-935-727-33
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PRIOR FILLING DATE: 2000-11-21
PRIOR FILLING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILLING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILLING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR FILLING DATE: 100/168,235
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SOFTWARE: PatentIn Ves
SEQ ID NO 33
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
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CURRENT FILING DATE: 2001-08-24
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TITLE OF INVENTION: Tumor Necrosis Factor Receptors
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PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
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TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICATION NUMBER: 60/131,270
                                                              TGTGGCCCGTGTCCACCGCCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
GTTGCTGAAACACCAACUTACCCATGGAGAGATGCTGAAACTGGTGAAAGACTGGTTTGT 797
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                                      TGTGGTCCATGTCCACCAAGACATTACACTCAATTTTGGAACTACCTGGAAAGATGTAGA 917
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67.7%;
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Pred. No. 8.6e-74;
0; Mismatches 263;
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TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REPERENCE: PF454P2
CURRENT APPLICATION WHRER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION WHRER: 60/303,224
PRIOR APPLICATION WHRER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR FILING DATE: 2000-11-21
PRIOR FILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/134,734
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR PRILNG DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
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US-09-935-727-3
Sequence 3, Application US/09935727
Patent No. US20020150583A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACACAGGGGAGCGGCTGGTGTGC
                                                                                                                                                                                                                                                                                                                                                               Score 387.4; DB 10; Length 1667;
Pred. No. 8.8e-73;
0; Mismatches 1; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCG
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR PILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 28, Application US/09935727; Patent No. US20020150583A1
                                                                                                                                                                                                                                                                                                                                                                  47.78;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 79.6
Matches 534; Conservative
                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 GGTACCAGGAG 535
                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS.;
; LOCATION: (73)..(582)
US-09-935-727-3
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US-09-935-727-28
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PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR PPLICATION NUMBER: 60/168,235
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR APPLICATION NUMBER: 60/131,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 533; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: intron
LOCATION: 425-560
NAME/KEY: intron
LOCATION: 756-1512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1997-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/303,224 PRIOR FILING DATE: 2001-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PF454P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLE OF INVENTION: Tumor Necrosis Factor Receptors
337
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                                                             GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGGAGCGGCTGGTGTGC 60
                                   GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCCGGGTGAGAGCTGGGCGAGGGGAGGG 447
                                                                                                                 AACCGTGCCTGCCGCACCGCACCGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
                                                                                                                                             AACCGTGCCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
                                                                                                                                                                                               TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTRGAGCGCTGCCGC
                                                                                                                                                                                                                                                                                                                     TGTGGCCCGTGTCCACCGCGCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180
                                                                                                                                                                                                                                                                                                                                                                                                     GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCCACGACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGC 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 387; DB 10; Length 1796; Pred. No. 1.1e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels 136;
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APPLICANT: PITTI, ROBERT
APPLICANT: ROY, MARGARET A
APPLICANT: TUMAS, DANIEL B
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
FILE REFERENCE: P1134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1997-09-18
PRIOR PRICING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09896096A
Patent No. US20020061559A1
GENERAL INFORMATION:
APPLICANT: ASHKEMAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Unknown organism;
; NAME/KEY: unsure
; LOCATION: 42, 62, 73, 86, 98, 106, :
; OTHER INFORMATION: unknown base
US-09-896-096A-5
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LENGTH: 271
                                                                                                                                                                                 Matches
                                                                                                                                                                                              Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                 19
                                                      ACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGGGGAGGCGTGAGGAGGAGGCAC 220
GGGCTTGCCACGCCACCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACG
                                ANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGGGGAGCNTGAGGAGGAGGCAN 120
                                                                                                       GCCGAGACAGCCCCACGACGTGTGGCCCCGTGTCCACCGCGCNACTACACGCAGTTCTGGA 60
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                                                                                                                                                                               250;
                                                                                                                                                                                                Similarity
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                      73, 86, 98, 106, 120, 122, 153, 167, 184, 220, unknown base
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                                                                                                                                                                           Score 245.2; DB 10;
Pred. No. 3.8e-43;
0; Mismatches 21;
                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                               Indels
                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                 271;
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280
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6, 2003, 16:08:07

Search completed: January Job time : 63 secs

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                                                                      281 CTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCA 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Unknown organism

) NAME/KEY: unsure

) LOCATION: 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233

) OTHER INFORMATION: unknown base

US-09-894-924-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.2%; Score 245.2; DB 10; Length 92.3%; Pred. No. 3.8e-43; Live 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BOTSTEIN, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: DODGE, KELLY H.
APPLICANT: GUNNEY, AUSTIN.
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: TAMAS, DAVIELE B
APPLICANT: TUMAS, DAVIELE B
APPLICANT: TUMAS, DAVIELE B
APPLICANT: TUMAS, DAVIELE B
APPLICANT: ROY, WARGARET A
APPLICANT: ROY, WARGARET B
APPLICANT: TUMOD, WILLIAM I.
TITLE OF INVENTION DCR3 POLYOPO948
FRIOR APPLICATION NUMBER: US 60/059,288
FRIOR APPLICATION NUMBER: US 60/059,288
FRIOR APPLICATION NUMBER: US 60/059,288
FRIOR APPLICATION NUMBER: US 60/059,640
FRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CCCCCAGCCAGAACACGCATGCAAAGCCGTG 271
                                                                                                                                                             341 CCCCCAGCCAGAACACGCCAGTGCCAGCCGTG 371
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                                                                                                                                                                                                      241 CCCCCAGCCAGAACACGCATGCAAAGCCGTG 271
                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09894924
Patent No. US20020065210Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.33
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                 RESULT 15
US-09-894-924-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221
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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO spool/US09936024/runat 06012003 111607 12130/app query.fasta_1.455
-Q=/cgn2 1/USPTO spool/US09936024/runat_06012003 111607 12130/app query.fasta_1.455
-DB=GenEmbl -QFMT_fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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2: gb htg:
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6: gb pat:*
7: gb pat:*
7: gb pt:*
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Ygapop 10.0 , X
Ygapop 6.0 , I
Delop 6.0 , I
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Copyright (c) 1993 - 2003 Compugen Ltd.
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
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35: em_htg_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

45	44		42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	110		ρα	o ~	) <b>o</b> n	· UT	4.	ω	2		Result No.
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ALIGNMENTS

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PAT 03-JUL-2001
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1 (bases 1 to 813)
1u. J. and Witcher, D. R.
Improving stability of flint through o-linked glycosylation Patent: WO 0142463.A 2 14-JUN-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
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ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp
                                             CGCGGGCCTTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGAC
                                                                            GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu
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a _298 c _267 g _126
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Sequence 2 from Patent W00142463.
AX167223
AX167223.1 GI:14596692
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AUTHORS
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            PAT 11-MAY-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bumol, T.F. and Cohen, F.J.
Therapeutic applications of flint polypeptides
Patent: WO 0128582-A 2 26-APR-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
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AX119833 GI:14036593
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REFERENCE 1 (bases 1 to 903) AUTHORS YU,K.Y., KWON,B., N.J., Zhai,Y., Ebner,R. and KWON,B.S. TITLE A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis JOURNAL J. Biol. Chem. 274 (20), 13733-13736 (1999)  MEDLINE 99253915  MEDLINE 99253915  MEDLINE 99253915  AUTHORS TOURNAL J. Biol. Chem. 274 (20), 13733-13736 (1999)  REFERENCE 2 (bases 1 to 903)  REFRENCE 2 (bases 1 to 903)  AUTHORS KWON,B.S. and Yu,K.Y.  TITLE Jurect Submitseion  JOURNAL Submitted (10-MAR-1999) Micro/Immunol, Indiana University, 635  FEATURES  Barnhill Drive, Indianapolis, IN 46202, USA  FEATURES  BOURCE 1.903	903 k necrosis fa 938	261 ArgSerValArgGluArgPheLeuProValHis 271 	Qy 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240	Db 541 GAGTGTGAGCGTCATCGACTTTGTGGCTTTTCCAGGACATCTCCATCAAGAGGCTG 600  Qy 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220	Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180	Oy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160	121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerSerGluGlnCysGln 1	Qy 101 AlaSerCysProProGlyAlaGlyVallleAlaProGlyThrProSerGlnAsnThrGln 120	Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100	Oy 61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80	Db 121 TGTGGCCCGTGTCCACCGCCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC 180

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Homo sapiens M68E mRNA, alternatively spliced, complete cds.
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1 (bases 1 to 1048)
Bai,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X., Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austin,C.P. and Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
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Sequence 1
AX082868
Ntr3, a member of the tnf-receptor supergene family Patent: WO 0110908-A 1 15-FEB-2001; Amgen Inc. (US)
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Mammalia; Eutheria;
1 (bases 1 to 1055)
                                                                                         AX082868.1
                                                              Homo sapiens
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Patent WO0110908.
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Primates;
                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                   GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu
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VAFQDISIKLQRLLQALDAEGWGFTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
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                 LeuAsnValProGlySerSerSerHis 160
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Pitti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,
Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,
Goddard,A.D., Botstein,D. and Ashkenazi,A.
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Pitti,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C., Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T., Godowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L., Goddard,A.D., Botstein,D. and Ashkenazi,A.

Genomic amplification of a decoy receptor for Fas ligand in lunc
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis
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Submitted (04-NOV-1998) Molecular
San Francisco, CA 94080, USA
Location/Qualifiers
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/db_xref="G1:4106878"
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83SSSECCOPHRNCTALGLALAVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDF
VAFQDISIKRLQRLLQALEAPEGMGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRL
LQALRVARMPGLERSVERFFLFVH"
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/product="decoy_receptor"
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/translation="MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETG
FRLVCAQCPPGTFVQRPCRRDSPTTGPCPPRHYTOFWNYLERCRYCNVLCGEREEEA
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VAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRTTELLGAQDGALLVRL
LOALRVARMPGLERSVRERFLPVH"
                                                       necrosis factor receptor superfamily,
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Conteat: MGC help desk
Conteat: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens, tumor necrosis factor receptor superfamily, member 6b, decoy, clone MGC:9587 IMAGE:3886635, mRNA, complete cds. BC017065 BC017065.1 GI:16877637
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (05-MOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                          gacaccererecaccacerecacerecerececereaceaccagegraceagagereag
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                                     AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu
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/tissue_type="Lung, carcinoma, large cell
undifferentiated."
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/db_xref="LocusID:8771"
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Homo sapiens
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 28 Row: o Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1479016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., I
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center
Center code: BCM-HGSC
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BC034349
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                           109
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/clone="MGC:21079 IMAGE:4752507"
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             GAGTGTGAGCGTGCCTTTGTGTGTTTTCCAGGACATCTCCCATCAAGAGGCTG
                                               GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly
                                                             CAGCGGCTGCTGCTGCCTCGAGGCCCCCGGAGGGCTGGGGTCCGACACCAACGGGGG
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Polynucleotide encoding TNFL1
Patent: US 6297367-A 18 02-OCT-2001;
Location/Qualifiers
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AR171895.
AR171895.1 GI:17910845
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/ Organism="Homo sapiens"
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/ Decell and protein product"
/ Codon start=1
/ Protein id="CAC07698.1"
/ Ab_xref="G1:10042432"
/ LTanslation="WRALEGFGISLICLVLALPALLPVPAVRGVAETPTYPWRDAETG
/ LTanslation="WRALEGFGISLICLVLALPALLPVPAVRGVAETPTYPWRDAETG
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/ LTANSlation="WRALEGFGISLICLVLALPALLPVPAVRGVETPTYPWRDAETG
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/ LTANSlation="MRACHERPTY"
/ ACHATHNRACRETGFFAHAGFGISHARPTYGFGISHARPTAGFGISHARPTAGFGISHARPTAGFGISHARPTAGFGISHAVIDF
/ VARQDISTIRRIQALIQALEAPEGWGPTPRAGRAALQIKLRRRLTFELLGAQDGALLVRL
/ LQALRAVARWGGIERSYRERFLYH"
/ A92 c 371 g 211 t
        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1168)
Kroeger, B.
Receptor from the superfamily of tnt-receptors from the human lung Patent: WO 9946376-A 1 16-SEP-1999;
BASF AG (DE); KROEGER BURKHARD (DE)

Location/Qualifiers
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                                                                                                                                   Direct Submission
Submitted (21-DEC-1999) WP26A-1000, Merck Research
Summeytown Pike, West Point, PA 19403, USA
Location/Qualifiers
                                                                                                                                                                                                                                                        Overexpression of M68/DcR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene
                                                                                                                                                                                                                                                                                 Bai, C., Connorry, B., ....
Sandig, V., Soderman, A.,
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Mammalia; Eutheria;
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                                                                  /cell_type=435. .1337
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                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Austin,C.P.
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Percent Similarity:
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Query Match:
DB: US-09-936-024-1 (1-271) AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln AACCGTGCCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg GCCCAGTGCCCCCCAGGCACCTTTGTGCAGCGGCCGTGCCGGCGAGACAGCCCCACGACG GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGGAGCGGCTGGTGC ArgSerValArgGluArgPheLeuProValHis 271 GAGTGTGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG GACACCCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAG CCCCACCGCAACTGCACGGCCCTGGGCCCTGAATGTGCCAGGCTCTTCCTCCCAT TGCCAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC Similarity: CTGCTGGTGCGGCTGCTGCAGGCGTGGCCGTGGCCAGGATGCCCGGGCTGGAG 6.79e-64 1491.00 100.00% 100.00% 100.00% 9 x AF217793 (1-1428)Length:
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Conservative:
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Gaps: 1428 271 0 0 240 1241 1121 1061 1001 140 40 260 220 200 180 160 941 881 120 821 100 761 80 701 60 641

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Prediction of the coding sequences of unidentified human genes.
XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 6 (3), 197-205 (1999)
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DDLDKVLAVLAALTTAKPEDPPLLHRFSMFVRPHHKQRFSQTCTDLTGRPYPCMBPP
GPQEBRLAVPVLTHRAPQPPSRESKTGKTQSKI SSFLRQRPAGTGGEDAGFSQ
SSGPPHGAAAEWGEPHGRD.AQQQXTGAPGGPLAGFSQC
SSGPPHGAAAEWGEPHGRD.AQQQXTGAPGGPLSACCVCQCCGAEDVVPFCCPRCDF
ORCQACWQRHLQASRMCPACHTASRKQSVMQVFWPEGPHKDHEGAAGGARPVAAVPGVGA
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YRQDASRAVNQALGRVIRHRQDYGAVFLCDHRFAFADARAQLPSWVRPHVRVYDNFGH
VIRDVAQFFRVAERTWPRAFAATAPSYRGEDAVSEAKSPGFFFSTRAKSLDLHVPS
LKQRSSGSPAAGDPESSLCYPEDFVPARQRPRGLLAALEHSEQRAGSPGEEQAHSC
STLSLLSEKRRAEEPRGGRKK. RLVSHPEEPVAGAQTDRAKLFWVAVKQELSQANFAT
FTQALQDYKGSDDFFALAACLGPLFAEDPKKHNLLQGFYQFVRPHKQQFEEVCIQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, On May 9, 2002 this sequence version replaced gi:5689512: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="brain"
/clone lib="pBluescriptII SK plus"
/note="This sequence was obtained by subcloning of the DN fragments derived from two cDNA clones (1 - 834 was derived from https://product (Brain) and 835 - 4945 was derived from hk02589)."
                                                                                                                                                                                                                                                                                                                                                                         Chordata, Craniata, Vertebrata, Buteleostomi, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                      Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus clone:hk02589s1.
                                                               AB029011 4945 bp mRNA linear
Homo sapiens mRNA for KIAA1088 protein, partial cds.
AB029011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .4945
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/clone="hk02589s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 4945)
Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="KIAA1088"
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/gene="KIAA1088"
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                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                               DEFINITION
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VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
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MEDLINE
PUBMED
                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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Job time : 2909 secs

Page 13

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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SPTREMBL 21:*

SPTREMBL 21:*

Sp archea:*

Sp bacter:*

Sp fungi:*

Sp mamma

Sp mamma

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Sp pha

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Sp pha

Sp fungi:*

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1 VAETPTYPWRDAET
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764.915 Million cell upda
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sp_bacteria:*
sp_fungi:*
           sp_unclassified:*
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(c) 1993 - 2003
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Compugen Ltd
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Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12	11	10	9	8	7	o,	ທ	4.	w	N	,	Result No.
260	267.5	268.5	268.5	268.5	270.5	275	275	275	287	313.5	327	333.5	395	486.5	499.5	Score
17.4	17.9	18.0	18.0	18.0	18.1	18.4	18.4	18.4	19.2	21.0	21.9	22.4	26.5	32.6	33.5	Query Match I
348	349	349	349	349	349	348	348	348	651	433	482	459	302	285	285	Length
12	12	12	12	12	12	12	12	12	13	11	11	11	13	13	13	DB
057112	057099	057291	057102	057101	057100	057277	057108	057103	Q98SM6	Q91ZM6	088734	Q62327	OSU46D	98X06Ö	Q90W71	ij
057112 variola vir	O57099 monkeypox v	057291 monkeypox v	057102 monkeypox v	O57101 monkeypox v	O57100 monkeypox v	057277 monkeypox v	O57108 monkeypox v	O57103 monkeypox v		Q91zm6 rattus norv	O88734 mus musculu	Q62327 mus musculu	Q9pus0 salvelinus	Q90ys6 oncorhynchu	Q90w71 oncorhynchu	Description

4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
200	202	203.5	219.5	N	230.5	4	•	248.5	249.5	v	u	•	٠	•			•		257.5			259	260	260	6	260	260	260
13.4	13.5	13.6	14.7	15.2	15.5	16.4	16.5	16.7	16.7	16.8	16.9	17.0	7	17.0	17.1	17.1	17.3	17.3	17.3	17.3	17.3	17.4	7	7.	٠		17.4	
167	132	267	277	278	276	283	350	351	347	347	349	351	349	349	351	326	349	349	349	326	355	360	350	349	349	349	349	348
12	13	6	თ	σ	13	σ	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12
Q9DJL2	Q90Y18	002764	Q8WMQ2	Q8SQ34	Q9DDD2	Q9XSZ8	057123	057121	057115	057119	057109	057117	057305	057097	073559	057122	057284	Q8UYA7	057098	057120	Q85308	057118	057116	Q89118	289098	057111	057110	Q85407
Q9djl2 cowpox viru	Q90y18 salvelinus	002764 oryctolagus	٥ <u>٧</u>	sus	Q9ddd2 gallus gall	cercopit	O57123 cowpox viru	1 cowpox	UI	Θ	057109 variola vir			057097 camelpox vi	073559 cowpox viru				057098 camelpox vi	057120 cowpox viru	cowpox	057118 cowpox viru	cowpox	variola	variola	variola	5	

#### ALIGNMENTS

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Q90W71
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Best Local S
Matches 99
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Q90W71;
Q1_DEC-2001 (TrEMBLrel. 19, Created)
O1_DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1_JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative decoy receptor 3 protein.
Oncorrhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                     Receptor.
SEQUENCE
                                                                                                                                                                                                               Pleguezuelos O., Sécombes C.J.;
"Screening a rainbow trout (Oncorhynchus mykiss) cDNA library.";
Submitted (JUN-2001) to the EMEL/GenBank/DDBJ databases.
EMBL; AJ315137; CAC43329.1;
InterPro; IPR000561; EGF-like.
InterPro; IPR001568; TWFR_C6.
Pfam; PF00020; TNFR_C6; 3.

PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS0186; TNFR_NGFR_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q90W71
                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=HEAD KIDNEY;
62 CNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQC 121
                                                  26 AHTPTYIWRDDATGDSLTCDLCAPGTYLLKHCTKDRKSDCGPCPKSHYTEIWNYIERCQY 85
                                                                         2 AETFTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRY 61
                                                                                                                                      Similarity
                                                                                                                                                                                     285 AA; 31642 MW; FB75CFFC1E391AD0 CRC64;
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                               33.5%; Score 499.5; DB 13; Length 285;
37.1%; Pred. No. 5e-36;
tive 41; Mismatches 116; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                               (TrEMBLrel. 13,
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hes 82; Conserv
                                                                                                                                                                               SEQUENCE FROM N.A.
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                             01-MAY-2000
01-MAY-2000
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SEQUENCE
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86 CNRFCTADEIESVPCTQLHNRQCECKDGFYMTHGSCSRHRRCPPGEGVISNGTAHTDVKC 145
                               QPCPPGTFSASSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE 181
                                                                                        CERAVIDFVAFODISIKRLORLLOALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDG 241
                                                                                                         Liu L., Fujiki K., Dixon B., Sundick R.S.;
Liu L., Fujiki K., Dixon B., Sundick R.S.;
"Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine with a fractalkine-like stalk and a TNF decoy receptor using cDNA fragments containing AU-rich elements.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF401631; AAK91758.1;
InterPro; IPR000561; EGF-like.
InterPro; IPR000561; EGF-like.
Pfam; PF00020; TNFR_C6; 3.
SMART; SMO0181; EGF.; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 CNRFCTADELESVPCTQLHNRQCECKDGFYMTHGSCSRHRRCPPGEGVISNGTAHTDVKC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 QPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 EPCPVĞFFSAVSSSRKACQKFSVCPP--GRTTIPGNDMNDVYCSACRNG--SRTHEGQAI 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CERAVIDFVAFODISIKRLORLLQALEAPEGWGPTPRAGRAALOLKLRRRLTELLGAODG
                                                           146 EPCPVGFFSAVSSSRKACQKFSVCPPGG--TTIPGNDMNDVYCSACTNG--SRTHEGEAI
                                                                                                                                                                                                                                                                                                                                         Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 AA; 31795 MW; SE3BDIBGEFC6BABC CRC64;
                                                                                                                                                                                                                                                                                                                     Last annotation update)
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nes 118;
                                                                                                                                                                                                                                                                                                     sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.6%; Score 486.5;
36.3%; Pred. No. 6.9e
Live 41; Mismatches
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PROSITE; PS00652; TNPR NGFR 1; UNKNOWN 1.
PROSITE; PS50050; TNPR NGFR 2; 1.
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                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                    Oncorhynchus more 19, C. TremBirel. 19, L. 01-JUN-2002 (TremBirel. 19, L. TNF decoy receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 97; Conserv
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81 CAENQVVKQECSPSNNCECECKEGYYFNKKYEACIKHKECPPGYGANTTGTPHQDTECVQ 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 CGEREEEBARACHATHNRACRCRTGFFAHAGF--CLEHASCPPGAGVIAPGTPSQNTQCQP 123
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | | : | | | : : | | | : : | | | : : | | | : : : | | | : : : | | | : : : | | ELLPTFFIQLHQTMGIKRMRRL--AMRLPQEGGKKPLIG--AVMKRNRRGLHDFMNSWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;

"Amino acid variation in the tumor Necrosis factor receptor linked to autoimmune diabetes in NOD mice.";

Genomics 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 302;
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1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Murine tumour necroais factor receptor 2 protein (Fragment)
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
VCMI_TaxID=8038;
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                                                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                      Decoy TNF receptor.
Salvelinus fontinalis (Brook trout) (Brook char).
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Pred. No. 7.7e-27
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MEDLINE LOUISING N.T.

Bobe J., Goetz F.W.;

Bobe J. Reprod. 62:420-426(2000).

EMBL, AF156738; AAD56428.1; -.

HSSP; O14763; 1D4V.

INTERPO; IPR000561; BGF-1ike.

INTERPO; IPR000561; TNFR_66; 4.

SMART; SM00500; TNFR_66; 4.

SMART; SM005039; TNFR; 4.

PROSITE; PS01186; EGF 2; UNKNOWN 1.

PROSITE; PS00625; TNFR_NGFR_1; INKNOWN_1.
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O88734;
O1-NOV-1998 (Tr
O1-NOV-1998 (Tr
O1-JUN-2002 (Tr
P80 TNF-alpha r
                   EMBL;
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NON TER
VARIANT
EMBL; Y14619; CAA74969.1; JOINED. EMBL; Y14620; CAA74969.1; JOINED. EMBL; Y14621; CAA74969.1; JOINED. EMBL; Y14622; CAA74969.1; JOINED.
                                                                             SEQUENCE FROM N.A.

MEDLINE=98414512; PubMed=9740674;
Hurle B., Segade F., Rodriguez R., Ramos S.S.

"The Mouse Tumor Necrosis Factor Receptor 2 and Characterization of the two Transcripts. Genomics 52:79-98(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
VARIANT
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InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X76401; CAA53981.1;
HSSP; P19438; INCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mamm. Genome 5:726-727(1994).
                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Powell E.E., Wicker L.S., Peter "Allelic variation of the type
                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                   TNFR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95178848; PubMed=7873884;
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STRAIN=NOD;
                                                                                                                                                                                                                           NCBI_TaxID=10090;
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3 (TrEMBLrel. 08,
2 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                           (Mouse)
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345
                                                                                                                                                                                                                                                Chordata;
Rodentia;
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29.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Pred. No. 3e-21
43; Mismatches
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                                                                                                                                                                                                                                              Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                                                                             Ramos S.S., Lazo
                                                                                                                                                                                                                                                                                                                                                                                                                                       482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3e-21;
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                                                                                                                    Gene:
                                                                                                                          Genomic
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                                                                                                                                             P.S.;
                                                                                                                                                                                                                                                  Euteleostomi; 
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459;
                                                                                                                            Structure
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RESULT

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ID ZM6

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                                                                                  Query Match
Best Local S
Matches 59
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Best Local S
Matches 82
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EMBL; Y14679;
HSSP; P19438;
                                                                                                                                                                          Receptor.
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q91ZM6 PRELIMINARY; PRT; 433 AA.
Q91ZM6; Q91ZM6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Tumor necrosis factor receptor type II (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                               Pfam; PF00020; TNFR_C6; 4.

PROSITE; PS00652; TNFR_NGFR_1;

PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL; AF420214; AAL16021.1; -. InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                         "TNF-receptors p60 and p80 are constitutivel capillary endothelial cells and participate through the blood-brain barrier.";
                                                                                                                                                                                                                                                                                                                                                                                                                              Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., "TNF-receptors \mathfrak{p}60 and \mathfrak{p}80 are constitutively expressed by capillary endothelial cells and participate in TNF-alpha tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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32
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QMCCAKCPPGQYAKHFCNKTSDTVCADCAAGMFTQVWNHLHTCLSCSSSCSDDQVETHNC
                                     RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SI-----GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELLGAQDGALLVRLLQAL----RVARMPGLERSVRERFLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAPGTFSDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEEARACHATHNRACRCRTGFF----AHAGF----CLEHASCPPGAGVIAPGTPSQNTQCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82;
                                                                                  Similarity 35.:
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 29.3
82; Conservative
                                                                                                                                                                          1
433
433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482 AA;
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                                                                                                                                                                            433
45723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51106 MW;
                                                                                                        21.0%;
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                                                                                                                                                                            MW;
                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                  Score 313.5;
Pred. No. 1.6e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 327;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F6C15046B48FF83C
                                                                                                                                                                                                                                                                      UNKNOWN_2.
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                                                                                                                                                                               75736D835E72CA4A CRC64;
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                                                                                  1.6e-19;
ches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
.2e-20;
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                                                                                       Indels
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                                                                                                                                  Length
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; Murinae; Rat
                                                                                                                                  433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                     13;
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91
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NCBI_TaxID=10244;
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SEQUENCE
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 IEKTHCTALTDRECTCLSGTFQINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 DRAINQELICDKCPAGTYVSKHCTKSTLRECSPCPDGTFTKHENGIERCHPCKKPCELPM 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 EEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTFSQNTQCQPCPPGTFS 130
                  HATHNRACRCRIGFFA----HAG---FCLEHASCPPGAGVIAPGIPSQNTQCQPCPPGTF 129
                                               92 TKKQNRVCACNADSYCALKLHSGNCRQCMKLSKCGPGFGVARSRTSNGNVICSACAPGTF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 DAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGERE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monkeypox virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
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Best Local Similarity 33.5%; Pred. No. 5.2e-17;
Matches 54; Conservative 27; Mismatches 80; Indels
                                                                                                             SASSSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
                                                                                                                                       152 SDTTSSTDVCRPHRICSILA---IPGNASTDAVCASES--PTPSAVP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Bridgham J.T., Johnson A.L.;
"Expression of DR6 in the ovary ";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         057103;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tumor necrosis factor receptor II homolog.
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 DVPSSVMKCKTYTDCFGKNMVVVKRGTKESDNVCGSPASLP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 ASSSSSEQCOPHRNCTALGLALNVPGSSSHDTLCTSCTGFP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSS0017; DEATH DOWAIN; 1.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
PROSITE; PS50050; TNFR NGFR 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBDILLEG (FRAIZOU) LO LUE EMBL/DEN
HSSP; P19438; INCF.
INCEPTO; IPRO00488; Death.
INCEPTO; IPRO0395; Shal_channel.
INCEPTO; IPRO0395; Shal_channel.
INCEPTO; IPRO01368; TNFR_C6.
PÉam; PF00531; death; 1.
PÉam; PF00620; TNFR C6; 4.
SWART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2001 (TrEMBLrel. 18,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              Gallus galīus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                           Death receptor 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEOUENCE
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O57103
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3 NQVETRSCNITHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 REEEARACHATHNRACRCRTGFF----AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loparev V.N., Parsons J.M., Esposito J.J.; "DNA sequence analysis as a criterion for allocation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
Local Similarity 33.1%; Pred. No. 3e-16;
es 59; Conservative 29; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.4%; Score 275; DB 12; Length 3 33.1%; Pred. No. 3e-16; ive 29; Mismatches 82; Indels
                                                   Loparev V.N., Parsons J.M., Esposito J.J.;
"DNA sequence analysis as a criterion for allocation of
                                                                                                       orthopoxviruses to a particular species.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88142; AAB94367.1; -.
HSSP, 014763; 1D0G.
                                                                                                                                                                                                                                                                                                                                                                                            348 AA; 38184 MW; 34A5E668B27907B5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tumor necrosas factor receptor II homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                  Interpro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR, 2.
PROSITE; PS00052; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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Pfam; PF00020; TNFR_c6; 2.
MARAT; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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SEQUENCE FROM N.A. STRAIN=ZAIRE-1979;
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057277;
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Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
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EMBL; AF380138; AAL40460.1; -.
HSSP; O14763; IDOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U88543; AAB94378.1; -.
EMBL; U87841; AAB94358.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21592287; PubMed=11734207; Safron Shchelkunov S.N., Totmenin A.V., Babkin I.V., Safron Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling F Sandakhchiev L.S.; "Human monkeypox and smallpox viruses: genomic compaFEBS Lett. 509:66-70(2001).
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STRAIN=ZAIRE-1996 /96-17, AND ZAIRE-1996 / 96-16;

STRAIN=ZAIRE-1996 /96-17, AND ZAIRE-1996 / 96-16;

LOPATEV V.N., Parsons J.M., Esposito J.J.;

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monkeypox virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ZAIRE-96-I-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ZAIRE-96-I-16;
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                                                                                                                                                                                                                                          RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVNDTSCTRTTTTGLSESISTSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS
                                                                                                                                                        RESEARACHATHNRACRCRTGFF-----AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
                                                                                                                                                                                                               KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TaxID=10244;
PCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVNDTSCTRTTTTGLSESISTSE
                                                 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE
                                                                                                       NOVETRS CNTTHNRICECS PGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           necrosis
                                                                                                                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         PS00652; TNFR NGFR 1;
PS50050; TNFR NGFR 2;
348 AA; 38212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sis factor receptor II homolog (J2R) (J2L).
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 06, (TrEMBLrel. 21,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                             Score 275; DB 1
Pred. No. 3e-16;
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2.
54019521556C2D8F CRC64;
                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     DB 12;
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                                                                                                                                                                                                                                                                                                                    82;
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                                                                                                                                                                                                                                                                                                                                                                     Length 348;
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RESULT
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  RESULT 12
057101
ID 05710
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DT 01-JU
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DT 01-JU
DT Tumor
GN CRMB.
OS Wonke
OC Virus
OC Ortho
OX NCBI
RN (I)
RP SEQUE
RC STRAI
RA LOBAR
RT "DNA
RT Ortho
DR HSSP;
DR HSSP;
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O57100;
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SEQUENCE
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Tumor necrosis factor receptor II homolog.
Loparev V.N., Parsons J.M., Esposito J.J.; "DNA sequence analysis as a criterion for allocation of orthopoxviruses to a particular species."; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases EMBL; U87845; AAB94362.1; -.
                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "DNA sequence analysis as a criterion for allocation of orthopoxviruses to a particular species."; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=ZAIRE-1977;
                                                                                                                                                                                                                                                                                                 Monkeypox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2;
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                                                                                                                                                                                                                       NCBI_TaxID=10244;
                                                                                                                                                                                                                                                   Viruses; dsDNA viruses,
Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                  Tumor necrosis
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39; Conservative
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    06, Created)
    06, Last sequence update)
    21, Last annotation updatreceptor II homolog.

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9; Mismatches
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152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTTGLSESISTS 209
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
[1]
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=VARIOUS STRAINS;
Loparev V.N., Parsons J.M., Esposito J.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, U87942; AAB94369.1; --
EMBL; U87942; AAB94365.1; --
EMBL; U87994; AAB94366.1; --
EMBL; U87995; AAB94366.1; --
EMBL; U87995; AAB94366.1; --
EMBL; U87995; AAB94366.1; --
EMBL; U87995; AAB94368.1; --
HSSP; O14763; IDDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBD2C949ED2B8E7C CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tumor necrosis factor receptor II homolog.
                                                                                                                                                                                            Last sequence update)
Last annotation update)
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NCBI_TaxID=10244;
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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                                                                                                                                DB 12; Length 349;
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STRAIN=BENIN-1978;
Loparev V.N., Parsons J.M., Esposito J.J.;
Loparev enalysis as a criterion for allocation of the orthopoxylruses to a particular species.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                             Query Match 18.0%; Score 268.5; DB 12; Length Best Local Similarity 32.6%; Pred. No. 1.1e-15; Matches 59; Conservative 29; Mismatches 80; Indels
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                                                                                  Receptor.
SEQUENCE 349 AA; 38311 MW; 02F65B00CFB858BE CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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HSSP, O14763; 1D0G.
InterPro; IPR001368; TNFR.c6.
Pfam; PF00020; TNFR.c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00052; TNFR NGFR.1; 2.
PROSITE; PS50050; TNFR NGFR.2; 2.
Interpro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
SMART; SM00208; TNFR; 2.
PROSITE; PS00052; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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Matches 59; Conservative
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NCBL_TaxID=10244;
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STRAIN=SIERRA LEONE-1970;

XL Loparev V.N., Parsons J.M., Esposito J.J.;

YI "DNA sequence analysis as a criterion for allocation of the orthopoxviruses to a particular species.";

Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

RR EMBL; U87843; AAB94360.1; -.

RR HSSP; O14763; 1D0G.

InterPro; IPR001368; TMFR C6.

PR FIAN; PE00200; TMFR C6; 2.

RR PART; SM00208; TMFR NGFR 1; 2.

RR PROSITE; PS00552; TMFR NGFR 1; 2.

RR PROSITE; PS00550; TMFR_NGFR_2; 2.

RR PROSITE; PS00550; TMFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                     Query Match 17.9%; Score 267.5; DB 12; Length 349; Best Local Similarity 32.6%; Pred. No. 1.4e-15; Matches 59; Conservative 28; Mismatches 81; Indels 13; Gaps
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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q-/Ggn2 1/USPTO_Spool/US09936024/runat_06012003_111607_12141/app_query.fasta_1.455
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-bluman40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM-ext -HEABSIZE=500 -WINLEN=0 -MAXLEN=200000000
-USER=US09936024_0CGN 1 1 1349_0runat_06012003 111607_12141 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMĀP -LĀRĞEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPDF=6 -FGAPEXT=7
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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01 zo70e05.r 931 wt08b06. 544 xc33a03.	25673 Ze90h09. 61219 tq27cll. 771720 h171a02	33463 K-ESTO1 83914 xc25g02 14771 UI-H-BI 772727 UI-E-CC 7725 wl21a08 04999 UI-H-BI	9166 6014 3766 6014 8134 AGEN 8135 XW59 1440 XW59 2363 hi25 2363 hi25 743 as95h 3454 K-ES	18 K-EST004 18 K-EST004 46 K-EST004 46 K-EST004 85 UI-H-DT1 64 K-EST000 72 K-EST000 38 K-EST003 26 K-EST003	78006 60148978 39551 60203901 64298 BP230015 83241 xc07a04. 83247 60308330 38357 60308330	I821789 60303586 Q687526 AGENCOUR E878908 60149260 M767535 K-EST005 G679499 60262751 M680786 UI-E-E01	ription

# ALIGNMENTS

AUTHORS TITLE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BI821789	RESULT 1
I (pases I to III) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.	EST.	BI821789.1 GI:15933339	BI821789	mRNA sequence.	603035863F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176910 5',	BI821789 1118 bp mRNA linear EST 04-OCT-2001		

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US-09-936-024-1 (1-271) x BQ687526 (1-863)
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/organism="Homo sapiens"
/db_xer="Homo sapiens"
/db_xer="twan:9606"
/clone="lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age for lang, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyre Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMI1440 row: n column: 15
High quality sequence stop: 758.
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/ Stratagene) and Superscript II RT (Life Technologies) |
/ Note: this is a NIH_MGC Library |
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Manmalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 863)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2394 row. c column: 12
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AGENCOURT 8345883 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250691
5', mRNA Sequence.
BQ687526.1 GI:21812842
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480 CAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCCGGAGGGCTGGGGTCCGACACC
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Mismatches:
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.

1 (bases 1 to 617)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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601492609F1 NIH_MGC_69 Homo sapiens
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

ACCESSION

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BG679499 1037 bp mRNA linear EST 01-MAY-2001
602667514F1 NCI_CGAP_SKn4 Homo sapiens cDNA clone IMAGE:4752507 5',
mRNA sequence.
BG679499
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I (bases 1 to 1037)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMI0610 row: k column: 04

High quality sequence stop: 762.

Location/Qualifiers
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                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 572)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Frontier Korean EST Project 2001

L Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eocun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4470
BM767535 572 bp mRNA linear EST 04-MAR-2002
K.EGT0050015 SISNU5s2 Homo sapiens CDNA clone SISNU5s2-3-E03 5',
mRNA sequence.
BM767535
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Matches:
Conservative:
Mismatches:
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/lab_host="Top10F'"
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Plate: 3 row: E column: 03
High quality sequence stop: 572.
Location/Qualiflers
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|clone="$1$NU5s2-3-E03"
|clone_lib="$1$NU5s2"
|sex="F"
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BASE COUNT ORIGIN

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LeuGlyAla---GlnAspGlyAlaLeuLeuValArgLeu 247
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                                                                      ThrProArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeu
                                                                                                            AAGAAGGCTTGCAGGGGGTTGTGGCAGGCCCTTCCGAAGGCCCCGAGGGCTGGGGGTTCCG
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis
                                                                                                        CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg
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                             TGTGGCCCGTGTCCACCGCGCCACTACACGCAGTTCTGGAACTACCTGGAGCGCTGCCGC
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High quality sequence stop: 560.
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Plate: LLAM12112 row: n column: 15
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National Institutes of Health, Mammalian
Unpublished (1999)
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AGENCOURT 6424187 NIH MGC 67
5', mRNA Bequence.
BM480117
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/lab_host="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
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/organism="Homo sapiens"
/db.xerf="texon:9606"
/clone="Mul.E-E01-ajc-j-12-0-UI"
/clone="Mul.E-E01-ajc-j-12-0-UI"
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/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524 AGCTCAGAGCAGTGCCCACCGCAACTGCACCGGCCCTGGGCCTTGGCCCTCAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_LIB=U1-E-E01
TAG_TISSUE=human fetal eye
TAG_SEQ=CGCGTATACC"
1218 c 248 g 129 t
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Best Local Similarity:
Query Match:
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Pred. No.:
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Program for Rat Gene Discovery and Mapping
University of Iowa
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9265
Email: msoarce@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequenching by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Seq primer: M13 Forward
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cararrhini; Hominidae; Homo.
1 (bases 1 to 728)
Bonaldo, M. F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                        ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSis 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    913 AATCACACCACCTCCTTTGGCGCACCCAAATCCTCTGGCAGTTTCGCTTTTGCACGCCCC 972
AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln
                                                                                                              CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln
                                                                                                                                                                                                                                                                                                                                                                                                                               GACACCCTGTGCACCCGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAAGAGCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCCAGCCGTGCCCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGGCTCAGAGCAGCAGCAG
                                                                                                                                                                                                                                                                                                                              CCCCACCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCAT
                                                                                                                                                                                                                                                                                                                                                                                            AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAla-Gl
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AUTHORS
TITLE
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645 114

728 196 1 1

Length:
Matches:
Conservative:
Mismatches:
Indels:

134

525 154 465

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174

213

233

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BASE COUNT
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Best Local Similarity:
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SerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPro
                                                                                                                             SerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSer 135
                                                                                                                                                                                                                                                                                                                                                                  CysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGly
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                                                                                                                                                                                                                                                                                                                                 TGCCACGCCAC-CACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGT
                                                                                           TTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCCGGGCGTGATTGCCCCCGGGCACCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Inctyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 679)

II Homo:
II Homo:
III Homo:
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Location/Qualifiers
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Tissue Procurement: DCTD/DTP/Gazdar
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/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:3891908"
/clone_1ib="NIH MGC 69"
/clone_1ib="NIH MGC 69"
/tlssue_type="large_cell carcinoma, undifferentiated"
/lab host="DH108 (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Site_3: Sall; Cloned unidirectionally. Primer: Oligo dT.
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5', mRNA sequence.
BF339551
BF339551.1 GI:11286006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 874)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                     /clone_lib="NCI_CGAP_Brn64"
/tissue_type="glioblastoma with EGFR amplification
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer: Oli
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 299 c 301 g 145 t
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/clone="IMAGE:4186995"
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Best Local Similarity:

University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA Tel: 217 333 5998 Fax: 217 244 5617 Email: h-lewin@uiuc.edu Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center PHRAP suite. Cross_match from Mashington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length.	PCR PRIMETS FORWARD: TATACGACTCACTATAGGG BACKWARD: ATTAACCTCACTAAG Insert Length: 554 Std Error: 0.00 Plate: BP230015A20 row: G column: 11 Seq primer: AGCGGATAACAATTTCACACGGA High quality sequence stop: 554. FEATURES 1. 554 Corganism="Bos taurus" (Ab xref="taxon:9913" //lone="#P520015A20611"	/ Jab host="Femile"   Jacob Host="Femile"   Jab host="Philo"   Jab host="DHIOB"   Jab host="DHIOB"   Jab host="DHIOB"   Jab host="DHIOB"   Jab host="DHIOB"   Jab host="Only library was contributed by the Site 2: Not1; The CDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. " ORIGIN 76 a 213 c 184 g 81 t 6(9): 791-806. "	Alignment Scores:	Qy         2 AlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAla         21	Qy         42         GlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyr         61
Query Match:         63.15%         Indels:         14           DB:         2         2           US-09-936-024-1 (1-271) x BF339551 (1-874)         0         1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys         20           Qy         1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys         21           Db         185 GTGGCAGAAACACCCACCACCAGGGGGAGGGGGGGGGGG	41 305 61 365 81 81	Oy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120	605 CCCACCG-AGCTGGCCTGGGCCTCAATGTGCCTTTTCTCTCCTCTT 663  QY 161 ASpThrLeuCys-ThrSprcysThrdlyPheProLeuSerThrArgValProGlyAlaG1 180  164 AspThrLeuCys-ThrSprcysThrdlyPheProLeuSerThrArgValProGlyAlaG1 180  165 AspThrLeuCys-ThrSprcySThrdlyPheProLeuSerThrArgValProGlyAlaG1 180  166 AspThrLeuCys-ThrSprcySThrdlyPheProLeuSerThrArgCargAGTTGA 720  QY 180 uGlu-CysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLySArgL 200  171 TGAAGTGTGAGCGTGCTTTCTGAGTTTGTGGCTTCCAGGGACTCCCATCAAGAGGT 780	Qy         200 euGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaG 220           Db         781 GC	RESULT 10  AW464298  LOCUGS  DEFINITION  BP230015A20G11 Soares normalized bovine placenta Bos taurus CDNA  ACCESSION  AW464298

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                                                                 CTG---TTTCTGCTGGAGCACGCATCGTGTCCACCTGT-GCCGGCGTGATTGCCCCGGGC
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Clone distribution: NCI-CGAP clone distribution
Clone distribution: NCI-CGAP clone distribution
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michae
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortiu www-bio.llnl.gov/bbrp/image/image.html Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anatomy
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/clone lib="NCI CGAP CO21"
/tissue_type="moderately differentiated adenocarcinoma"
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B1838357
B1838357.1 GI
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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National Institutes of Health,
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(EcoRV site is destroyed upon cloning). Average size 1.5 kb, insert size range 1-2.5 kb. Librar normalized and enriched for full-length clones constructed by C. Gruber (Invitrogen). Research
                                                                     /nore="Organ: pooled pancreas and spleen; vector:
pCMV-SPORTS; Site1: Not1; Site2: ECORV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
                                                                                                                                            /clone="IMAGE:5222545"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
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mRNA linear EST 04-MAR-2002 CDNA clone S1SNU582-4-D01 5',
                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:8606"
/db_xref="taxon:8606"
/clone="InAAGB:275231"
/clone="lb="NCI GAPP_Lu28"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH108"
/note="Organ: lung, Vector: pCWV-SPORT6; Site_1: Sal1;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
a 177 c 199 g 102 t 2 others
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mismatches:
Indels:
                               Possible reversed clone: polyT not found Seq primer: -400F from Gibco High quality sequence stop: 410.
Location/Qualifiers
1. .600
ww-bio.llnl.gov/bbrp/image/image.html
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Matches:
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K-EST0049137 SISNUS82 Homo saplens
mRNA sequence.
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Fechnologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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   Note: this is a NIH MGC Library." 95 t 1 others
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Matches:
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a 224 c 171 g
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                                                                                           7.6e-61
836.00
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Best Local Similarity:
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Pred. No.:
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KEYWORDS
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AW262121/c
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AUTHORS
TITLE
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                                                                           ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys
                                                 GTGGCAGAAACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGT
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Kim, N.S.,
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Contact: Kim YS
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21C Frontier Korean EST Project 2001
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Plate: 4 row: D column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 Eoeun-dong Yuseong-gu, Tel: +82-42-860-4470
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Korea Research Institute of Bioscience
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m,N.S., Hahn,Y., Oh
,K.J., Cheong,J.E.,
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /incte="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NorI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF by electroporation method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription biotinylated single stranded RNA by in vitro transcription
                                                                                                                                                                                                                                                                                                                                                                                                                         electroporation method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToploF' with electroporation method."
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/sex="F"
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/cell_type="Lymphoblast-like"
/cell_line="SNU-5"
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/db_xref="taxon:9606"
/clone="S1SNU5s2-4-D01"
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Matches:
Conservative:
Mismatches:
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305-333, South Korea
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AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr

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REFERENCE
AUTHORS
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1 (bases 1 to 605)
Kim, N.S., Hahn, Y., Oh
Oh, K.J., Cheong, J.E.,
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| Location/Qualifiers
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21C Frontier Korean
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kim YS
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/note-"Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was adjusted to have about 60nt. The cDNA vector so circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The
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E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5, primer and N(dT)14 as 3 primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with
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Search completed: January 6, 2003, 12:04:15 Job time : 1972 secs

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1 VAETPTYPWRDAETGERLVC.....RVARMPGLERSVRERFLPVH 271
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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     GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd
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A60771
                    B32393

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gene ox40 protein
T-cell antigen 4-1
CD30 antigen precu
lymphocyte activat
nerve growth facto
nerve growth facto
nerve growth facto
apoptosis-mediatin
MEGF6 protein - ra
CD27 antigen precu
conadhesin - mouse
CD27 antigen precu
apoptosis-mediatin
hypothetical prote
FAS soluble protei
                                                                                                                                                                                                                                                                 hypothetical prote G2R protein - vari gene G4R protein - rabbi OX40 homolog - hum OX40 antigen precu B-cell activation T2 protein - myxom B cell-associated
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tumor necrosis fac
tumor necrosis fac
death receptor-6
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# ALIGNMENTS

A; Accession: A35007 A; Status: preliminary A; Molecule type: mRNA A; Residues: 116-140, pr, 142-195, 'R', 197-362, 'T', 364-461 <hel> A; Residues: 116-140, pr, 142-195, 'R', 197-362, 'T', 364-461 <hel> A; Cross-references: GB:M35857; NID:g339751; PIDN:AAAA3262.1; PID:g339752 A; Cross-references: GB:M35857; NID:g339751; PIDN:AAAA3262.1; PID:g339752 A; Coetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990 A; Title: Purification and partial amino acid sequence analysis of two distinct tumor nec; A; Reference number: A23666; MUID:91058048; PMID:2173696 A; Status: preliminary A; Molecule type: protein A; Residues: 23-40;65-69;136-141;300-306 <loe></loe></hel></hel>	A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A;Reference number: A48416; MUID:91370690; PMID:1966549  A;Recession: A48416  A;Status: preliminary A;Molecule type: mRNA; protein A;Residues: 23-461 <dem> A;Cross references: GB:563368; NID:9235648; PIDN:AAB19824.1; PID:9235649 A;Cross references: GB:563368; NID:9235648; PIDN:AAB19824.1; PID:9235649 A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371) R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990 A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstrat A;Reference number: A36007; MUID:90349572; PMID:2166946</dem>	A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-461 <smi> A;Cross-references: GB:M32315; NID:gl89185; PIDN:AAA59929.1; PID:gl89186 A;Cross-references: GB:M32315; NID:gl89185; PIDN:AAA36755.1; PID:gl89186 A;Cross-references: GB:M35594; GB:M38549; NID:gl39757; PIDN:AAA36755.1; PID:gl39758 A;Cross-references: GB:M55994; GB:M38549; NID:gl39757; PIDN:AAA36755.1; PID:gl39758 A;Cross-references: GB:M55994; GB:M38549; NID:gl39757; PIDN:AAA36755.1; PID:gl39758 A;Cross-references: GB:M55994; GB:M38549; NID:gl39757; PIDN:AAA36755.1; PID:gl39758 Cytokine 2, 231-237, 1990</smi>	A35356  A35356  tumor necrosis factor receptor 2 precursor [validated] - human  tumor necrosis factor receptor 2 precursor [validated] - human  N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  C;Species: Homo sapiens (man)  C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 08-Dec-2000  C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.  Science 248, 1019-1023, 1990  A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and v.  A;Reference number: A35356; MUID:90260639; PMID:2160731  A;Accession: A35356

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81; Conservative
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Matches 81; Conserv
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R;Engelmann, H.; Novick, D.; Wallach, D.

Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A;Reference number: A35010; MUID:90110215; PMID:2153136
                                                                                                                                                                     A; Residues: 27-31 < ENG>
R; Rebidues: 27-31 < ENG>
R; Kubnert, P.; Kemper, O.; Wallach, D.
R; Ribnert, P.; Sequencing and partial functional characterization of the 5' region A; Reference number: 138094; MUID:95121934; PMID:7821811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;3-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;10-162/Domain: NGF receptor repeat homology <NG3>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;120-162/Domain: NGF receptor repeat homology <NG3>
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A,Reference number: 148854; MUID:95178848; PMID:7873884
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C,Species: Mus musculus (house mouse)
C,Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVA----IPGNASMDA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 VCTSTS--PTRSMAPGAVHLPQPV----STRSQHTQPTPEPSTAPSTSFLLPMGPSP 249
                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 1-37 <RES>
A,Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 VAFTPYAP----EPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDST 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRH 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;262-279/Domain: transmembrane #status predicted <TMN>F;280-461/Domain: intracellular #status predicted <INT>F;11,1,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
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R;Powell, B.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A. Mamm. Genome 5, 726-727, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.8%; Score 340.5; DB 1; Best Local Similarity 29.7%; Pred. No. 1.9e-18; Matches 89; Conservative 43; Mismatches 115;
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tumor necrosis factor receptor type 2 precursor - mouse C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor A;Accession: B38634
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-474 <LEWA
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R;Godwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen!
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Reference number: A40254
A;Residues: 1-474 <GOO.
A;Cross-references: GB:N60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
A;Reference number: S54816
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A,Residues: 1-459 <RES>
A,Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C,Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology F,151-188/Domain: NGF receptor repeat homology <ANGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP----RAGRAALQLKLRRRLTELLGAQD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 HATHNRACRCRIGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                              37 QMCCAKCPPGQYVKHFCNKTSDTVCADCBASMYTQVWNQFRTCLSCSSSCSTDQVETRAC
                                                                                                                                                                                                                                                                                                                                                                    17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 PLD----QEPGPSQTPSILTSL-----GSTPIIEQSTKGGISLPIGLIVGVTSL----
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                                                                                                                                                                                    22.4%; Scort No. 6.3e 29.7%; Pred. No. 6.3e 110; we 43; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 22.3%; Score 332.5; DB 2; Il Similarity 29.7%; Pred. No. 7.7e-18; 81; Conservative 44; Mismatches 109;
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death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
C;Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine \( \)
A;Reference number: JC7705; MUID:21308433; PMID:11414698
                                                                                                                                                                     RESULT
JC7705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen A;Reference number: 154182; MUID:93252381; PMID:8486360
A;Accession: I54182
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R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision
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A;Map position: 12p13.3-12p13.1
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A; Residues: 1-435 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor necrosis factor receptor 2-related protein - human
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Best Local S
Matches 74
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                                                                                                                                                                                                                                                                                                                                                                                                                       110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
                                                                                                                                                                                                                                                                                                                                                                                                                     LEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EBEARACHATHNRACRCRTGFFAHAGFCLE--H----ASCPPGA-GVIAPGTPSQNTQCQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALLVRLLQAL----RVARMPGLERSVRERFLP 269
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                                                                                                                                                                                                                                                      LAVILPLAFFILLATVFSCIWKSHPSLCRKLGSLLK--RRPQGEGPNPVAG
                                                                                                                                                                                                                                                                                               ERAVIDEVAFQDIS----
                                                                                                                                                                                                                                                                                                                                   PCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE-PLPPEMSGTMLM
                                                                                                                                                                                                                                                                                                                                                                          PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPOHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICOLCRPCDPVMG-- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGER 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLLMLGLVNCIILVQRKKKPSCLQRDAKVPHVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 32.074; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.1%; Score 299.5; DB 2; 32.0%; Pred. No. 2.2e-15; tive 27; Mismatches 101;
                                                                                                                                                                                                                                                                                             -----IKRLQRLLQALEAPEGWGPTPRAG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from GB/EMBL/DDBJ
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                           vertebrates
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      RESULT
D72175
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A;Accession: JC7705
A;Molecule type: mRNA
A;Rosidues: 1-651 <BRI>
A;Cross-references: GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor tresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1-21/Domain: signal sequence #status predicted <SIG>F;52-196/Domain: extracellular cysteine-rich, ligand-binding F;52-196/Domain: transmembrane #status predicted <TVM>F;332-350/Domain: death domain #status predicted <DED>F;551-651/Region: conserved cytoplasmic #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
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C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-348 < MAS>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, Nature 366, 748-751, 1993
A;Tille: Potential virulence determinants in terminal regions A;Reference number: Z20488; MUID:94088747; PMID:8264798
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206
                                                                                                                    118 NTQCQPCPPGTFSASSSSSSSQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
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TSE
                                         GAE 180
                                                                                DVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL
                                                                                                                                                                                                       VLCGEREEEARACHATHNRACRCRTGFF-----AHAGFCLEHASCPPGAGVIAPGTPSQ 117
                                                                                                                                                                                                                                                PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN
                                                                                                                                                                                                                                                                                       PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN
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                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                      Similarity
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33.5%; Pred. No. 2e-14;
                                                                                                                                                                                                                                                                                                                              17.4%; Score 260; DB 2; 32.2%; Pred. No. 1.7e-12; tive 26; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L.I.; Qi, J.; Utterback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 651;
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                                                                                                                                                                  -SGHTSVG
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RESULT 9
B43692
Cypecies: rabbit fibroma virus
Cyspecies: rabbit fibroma virus
Cyspecies: rabbit fibroma virus, Shope fibroma virus
Cypecies: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
CyAccession: B43692, A.M.; McFadden, G.
Virology 160, 20-30, 1987
Virology 160, 20-30, 1987
AyTitle: Tumorispenic poxviruses: genomic organization and DNA sequence of the telomeric AyReference number: A43692; MUID:87321103; PMID:2820128
AyAccession: B43692
AyAccession: Preliminary
AyMolecule type: DNA
AyResidues: 1-325 <upre>CMD AyAccession
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: 137552
R;Latza, U; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fona:
Bur. J. Immunol. 24, 677-683, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 VLCGEREEEARACHATHNRACRCRTGFF----AHAGFCLEHASCPPGAGVIAPGTPSQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 LCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGHLSESQPCD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN
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C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
                                                                                                                              receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.7%; Score 234.5; DB 2; 32.9%; Pred. No. 1.4e-10;
A; Experimental source: strain India-1967, ssp. major C;Genetics:
A;Gene: GR.
C;Superfamily: myxoma virus T2 protein; NGF receptor F;32-66/Domain: NGF receptor repeat homology <NGF>F;68-109/Domain: NGF receptor repeat homology <NGS>F;110-151/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                     ; Score 260; DB 2;
; Pred. No. 1.7e-12;
26; Mismatches 90
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                                                                                                                                                                                                                                                                                                                 17.4%;
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Best Local Similarity
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Matches 52; Conserv
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OX40 homolog - human
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C; Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 23-Mar-2001
R; Blinov, V.M.
submitted to GenBank, November 1992
A; Recession: Dis658
A; Ratus: preliminary
A; Molecule type: DNA
A; Reperimental source: strain India-1967, ssp. major, isolate Ind3
A; Cross-references: GB: X69198; NID: 9456758; PIDN: CAA49137.1; PID: 9457087
A; Experimental source: strain India-1967, ssp. major, isolate Ind3
A; Rivolykhalov, A.A.; Blinov, V.W.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.B.; Frol submitted to the EMBL Data Library, April 1992
A; Reference number: $46888
A; Reterence number: $46888
A; Reterence number: $46888
A; Reterence number: $46888
A; Reterence spreliminary
A; Molecule type: DNA
A; Resperimental source: EMBL: X67117; NID: 9516428; PIDN: CAA47540.1; PID: 9516449
A; Experimental source: strain India-1967, isolate Ind3
B; Scholelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
B; Richelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
                                                                                                                                              R.;Abcelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998
A.;Bestription: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Reference number: A72150
A;Reference number: A72156
A;Status: preliminary
A;Residus: preliminary
A;Residus: 1-349 < cshC>
A;Residus: 1-349 < cshC>
A;Residus: 1-349 < cshC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A;Cross-references: strain Garcia-1966
C;Genetics:
A;Genetics:
A;Genetics
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A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A;Reference number: S32385; MUID:93202281; PMID:8384129
A;Accession: S32385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
;
                                    C;Spēcies: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 146
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variola minor virus (strain Garcia-1966)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 17.4%; Score 260; DB 2; Best Local Similarity 32.2%; Pred. No. 1.7e-12; Matches 59; Conservative 26; Mismatches 90;
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A;Residues: 31-168 <SHC>
A;Cross-references: EMBL:X69198
                                                                                                                 Accession: D72175
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A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment A;Reference number: I37552; MUID:94170844; PMID:7510240 A;Accession: I37552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-271 < MAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Characterization of the MRC OX40 antigen of activated A; Reference number: S12783; MUID:90214614; PMID:2157591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Mallett, S.; Fossum, S.; Barclay, A.N. EMBO J. 9, 1063-1068, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change C;Accession: S12783; S08036
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RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S12783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N; Alternate names: nerve growth factor receptor homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OX40 antigen precursor - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35
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                                                                                                                                                                                                                                                                            σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECERAVIDFVAFQDISIKRLQRLLQALEAPEGW-----GPTPR-----AGRAALQLKLRR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTS---CTGFPLSTRVPGAE 180
                                                              LGVDCVPCPPGHF - - SPGSNQACKPWTNCTLSGKQIRHPASNSLDTVC
                                                                                                                                                                                       VLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGT-PSQNT---
                                                                                                                                                                                                                                  TYP----SGHK-CCRECOPGHGMVSRCDHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCN
                                                                                                                                                                                                                                                                            TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRSG--SERKQLCTATQDTVCRCRAG-----TQPLDSYKPG------VDCAP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN
                                                                                                    ---QCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPPGHF--SPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPSNDR-----CCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCN 88
                                                                                                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.5%;
                                                                                                                                                                                                                                                                                                                                           14.2%; Score 211.5; DB 2; 31.5%; Pred. No. 6.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLG
                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 215.5; DB 2
Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104; Indels
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                 ----PGTQPRQDSSHK 117
                                                                                                                                                                                                                                                                                                                                                               Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 277;
                                                            163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:g57831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:g472958
                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            positive T lymphocyte
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A60771

B-cell activation protein CD40 precursor - human

N;Alternate names: B-cell surface antigen Bp50

C;Species: Homo sapiens (man)

C;Date: 03-Jun-1993 #sequence revision 03-Feb-1994 #text_change 21-Jul-2000

C;Accession: S04460; A60771

C;Accession: S04460; A60771

R;Stamenkovic, I.; Clark, E.A.; Seed, B.
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1;
A;Cross-references: GB:M95181; GB:M37976; NGF receptor repeat homology
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;106-147/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                       T2 protein - myxoma virus (strain Lausanne)
c;Species: myxoma virus
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
C;Accession: A40566
R;Upton, C; Macen, J.L.; Schreiber, M.; Mcfadden, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXYN>
F;19-215/Domain: transmembrane #status predicted <CYMN>
F;194-215/Domain: intracellular #status predicted <CYMN>
F;1953,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                           Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology
A;Reference number: A40566; MUID:91335768; PMID:1651597
A;Accession: A40566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like A;Reference number: A60771; MUID:89093941; PMID:2463309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to A;Reference number: S04460; MUID:89356608; PMID:2475341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:CD40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A60771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:215268; OMIM:109535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-277 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAFEKCHPWTSCETKDLVVQQAGTNKTDVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSSEQCOPHRNCTALGLALNVPGSSSHDTLC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ET--DTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HATHNRACRCRTGEFAHA---GECLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.2%;
30.5%;
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Pred. No. 7.1e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186
                  (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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stroem, P.;
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                                                                                                                                                                    PID: g332310
                                                                                                                                                                                                                                                                                                                         tumor necrosis
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Query Match

14.18;

Score 210.5;

DB 1;

Length 326;

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Search completed: January
Job time : 39 secs
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 HATHNRACRCRIGFFA---HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATHNRACRCRIGFFA----HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA 131
                                                                                                                                                                                                                                                                                          20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARAC 76
                                                                                                                                                                 38 LCCTSCPPGSYASKLCGPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHLSESQSCD 97
                                                                                                   18 LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEARACH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 CDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGT-
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                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell-associated surface molecule CD40, long splice form
                                 80;
                                                                                                                                                                                                                                                                                                                                                                                              SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVSSTETCTSSFNYISVEFNL----YPVNDTSCTTTAG 190
   No. 9.1e-09;
                                 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLFEKCYPWTSCEDKNLEVLOKGTSQTNVIC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 SSSEQCOPHRNCTALGLALNVPGSSSHDTLC 164
   Pred.
30.4%;
                                        Conservative
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   Best Local Similarity
                                            Matches
                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                                 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157
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R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell in A;Reference number: 148700; MJID:94044750; PMID:8228223
                                                                                                                                                                                                                                                       A; Residues: 1-272 <RES>
A; Cross-references: EMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
A; Cross-references: EMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
B. T. T. Immunol. 25, 926-930, 1995
A; Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A; Reference number: 148334; MUID:95255413; PMID:7737295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Residues: 1-14,'G',16-272 <RE2>
A,Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 HRSG--SELKQNCTPTQDTVCRCR--------PGTQPRQDSGYK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 VLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGT-PSQNT--- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.0%; Score 194.5; DB 2; Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 --- QCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 LGVDCVPCPPGHF--SPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Generics:
A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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